

μL of the diluted conjugate was added to each well and incubated for 30 minutes at room temperature. Following incubation, the wells were washed five times with PBS/0.1% Tween 20™. 100 μL of tetramethylbenzidine peroxidase (TMB) substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) was added, undiluted, and 5 incubated for about 15 minutes. The reaction was stopped with the addition of 100 μL of 1 N H₂SO₄ to each well, and the plates were read at 450 nm.

Figure 4 shows the ELISA reactivity of two recombinant antigens isolated using method A in Example 3 (TbRa3 and TbRa9) with sera from *M. tuberculosis* positive and negative patients. The reactivity of these antigens is 10 compared to that of bacterial lysate isolated from *M. tuberculosis* strain H37Ra (Difco, Detroit, MI). In both cases, the recombinant antigens differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 56 out of 87 positive sera, and TbRa9 detected 111 out of 165 positive sera.

Figure 5 illustrates the ELISA reactivity of representative antigens 15 isolated using method B of Example 3. The reactivity of the recombinant antigens TbH4, TbH12, Tb38-1 and the peptide TbM-1 (as described in Example 4) is compared to that of the 38 kD antigen described by Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989. Again, all of the polypeptides tested differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbH4 20 detected 67 out of 126 positive sera, TbH12 detected 50 out of 125 positive sera, 38-1 detected 61 out of 101 positive sera and the TbM-1 peptide detected 25 out of 30 positive sera.

The reactivity of four antigens (TbRa3, TbRa9, TbH4 and TbH12) with sera from a group of *M. tuberculosis* infected patients with differing reactivity in the 25 acid fast stain of sputum (Smithwick and David, *Tubercle* 52:226, 1971) was also examined, and compared to the reactivity of *M. tuberculosis* lysate and the 38 kD antigen. The results are presented in Table 3, below:

TABLE 3
REACTIVITY OF ANTIGENS WITH SERA FROM *M. TUBERCULOSIS* PATIENTS

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-2	++++	1.853	0.634	0.998	1.022	1.030	1.314
Tb01B93I-19	++++	2.657	2.322	0.608	0.837	1.857	2.335
Tb01B93I-8	+++	2.703	0.527	0.492	0.281	0.501	2.002
Tb01B93I-10	++	1.665	1.501	0.685	0.216	0.448	0.458
Tb01B93I-11	+++	2.817	0.697	0.509	0.301	0.173	2.608
Tb01B93I-15	+++	1.28	0.283	0.808	0.218	1.537	0.811
Tb01B93I-16	+++	2.908	>3	0.899	0.441	0.593	1.080
Tb01B93I-25	---	0.395	0.131	0.335	0.211	0.107	0.948
Tb01B93I-87	++	2.653	2.432	2.282	0.977	1.221	0.857
Tb01B93I-89	--	1.912	2.370	2.436	0.876	0.520	0.952
Tb01B94I-108	--	1.639	0.341	0.797	0.368	0.654	0.798
Tb01B94I-201	--	1.721	0.419	0.661	0.137	0.064	0.692
Tb01B93I-88	--	1.939	1.269	2.519	1.381	0.214	0.530
Tb01B93I-92	--	2.355	2.329	2.78	0.685	0.997	2.527
Tb01B94I-109	--	0.993	0.620	0.574	0.443	0.5	2.558
Tb01B94I-210	++	2.777	>3	0.393	0.367	1.004	1.315
Tb01B94I-224	++	2.913	0.476	0.251	1.297	1.990	0.256
Tb01B93I-9	+	2.649	0.278	0.210	0.140	0.181	1.586
Tb01B93I-14	+	>3	1.538	0.282	0.291	0.549	2.880
Tb01B93I-21	+	2.645	0.739	2.499	0.783	0.536	1.770

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-22	+	0.714	0.451	2.082	0.285	0.269	1.159
Tb01B93I-31	+	0.956	0.490	1.019	0.812	0.176	1.293
Tb01B93I-32	-	2.261	0.786	0.668	0.273	0.535	0.405
Tb01B93I-52	-	0.658	0.114	0.434	0.330	0.273	1.140
Tb01B93I-99	-	2.118	0.584	1.62	0.119	0.977	0.729
Tb01B94I-130	-	1.349	0.224	0.86	0.282	0.383	2.146
Tb01B94I-131	-	0.685	0.324	1.173	0.059	0.118	1.431
AT4-0070	Normal	0.072	0.043	0.092	0.071	0.040	0.039
AT4-0105	Normal	0.397	0.121	0.118	0.103	0.078	0.390
3/15/94-1	Normal	0.227	0.064	0.098	0.026	0.001	0.228
4/15/93-2	Normal	0.114	0.240	0.071	0.034	0.041	0.264
5/26/94-4	Normal	0.089	0.259	0.096	0.046	0.008	0.053
5/26/94-3	Normal	0.139	0.093	0.085	0.019	0.067	0.01

Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 23 out of 27 positive sera, TbRa9 detected 22 out of 27, TbH4 detected 18 out of 27 and TbH12 detected 15 out of 27. If used in combination, these four antigens would have a theoretical sensitivity of 27 out of 27, indicating that these antigens should complement each other in the serological detection of *M. tuberculosis* infection. In addition, several of the recombinant antigens detected positive sera that were not detected using the 38 kD antigen, indicating that these antigens may be complementary to the 38 kD antigen.

The reactivity of the recombinant antigen TbRa11 with sera from *M. tuberculosis* patients shown to be negative for the 38 kD antigen, as well as with sera from PPD positive and normal donors, was determined by ELISA as described above.

The results are shown in Figure 6 which indicates that TbRa11, while being negative with sera from PPD positive and normal donors, detected sera that were negative with the 38 kD antigen. Of the thirteen 38 kD negative sera tested, nine were positive with TbRa11, indicating that this antigen may be reacting with a sub-group of 38 kD antigen negative sera. In contrast, in a group of 38 kD positive sera where TbRa11 was reactive, the mean OD 450 for TbRa11 was lower than that for the 38 kD antigen. The data indicate an inverse relationship between the presence of TbRa11 activity and 38 kD positivity.

The antigen TbRa2A was tested in an indirect ELISA using initially 50 µl of serum at 1:100 dilution for 30 minutes at room temperature followed by washing in PBS Tween and incubating for 30 minutes with biotinylated Protein A (Zymed, San Francisco, CA) at a 1:10,000 dilution. Following washing, 50 µl of streptavidin-horseradish peroxidase (Zymed) at 1:10,000 dilution was added and the mixture incubated for 30 minutes. After washing, the assay was developed with TMB substrate as described above. The reactivity of TbRa2A with sera from *M. tuberculosis* patients and normal donors is shown in Table 4. The mean value for reactivity of TbRa2A with sera from *M. tuberculosis* patients was 0.444 with a standard deviation of 0.309. The mean for reactivity with sera from normal donors was 0.109 with a standard deviation of 0.029. Testing of 38 kD negative sera (Figure 7) also indicated that the TbRa2A antigen was capable of detecting sera in this category.

TABLE 4
REACTIVITY OF TBRA2A WITH SERA FROM *M. TUBERCULOSIS* PATIENTS AND FROM
NORMAL DONORS

25

Serum ID	Status	OD 450
Tb85	TB	0.680
Tb86	TB	0.450
Tb87	TB	0.263
Tb88	TB	0.275
Tb89	TB	0.403
Tb91	TB	0.393
Tb92	TB	0.401

Tb93	TB	0.232
Tb94	TB	0.333
Tb95	TB	0.435
Tb96	TB	0.284
Tb97	TB	0.320
Tb99	TB	0.328
Tb100	TB	0.817
Tb101	TB	0.607
Tb102	TB	0.191
Tb103	TB	0.228
Tb107	TB	0.324
Tb109	TB	1.572
Tb112	TB	0.338
DL4-0178	Normal	0.036
AT4-0043	Normal	0.126
AT4-0044	Normal	0.130
AT4-0052	Normal	0.135
AT4-0053	Normal	0.133
AT4-0062	Normal	0.128
AT4-0070	Normal	0.088
AT4-0091	Normal	0.108
AT4-0100	Normal	0.106
AT4-0105	Normal	0.108
AT4-0109	Normal	0.105

The reactivity of the recombinant antigen (g) (SEQ ID NO: 60) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. Figure 8 shows the results of the titration of antigen (g) with four 5 *M. tuberculosis* positive sera that were all reactive with the 38 kD antigen and with four donor sera. All four positive sera were reactive with antigen (g).

The reactivity of the recombinant antigen TbH-29 (SEQ ID NO: 137) with sera from *M. tuberculosis* patients, PPD positive donors and normal donors was determined by indirect ELISA as described above. The results are shown in Figure 9. 10 TbH-29 detected 30 out of 60 *M. tuberculosis* sera, 2 out of 8 PPD positive sera and 2 out of 27 normal sera.

Figure 10 shows the results of ELISA tests (both direct and indirect) of the antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors and with a pool of sera from *M. tuberculosis* patients. The mean

OD 450 was demonstrated to be higher with sera from *M. tuberculosis* patients than from normal donors, with the mean OD 450 being significantly higher in the indirect ELISA than in the direct ELISA. Figure 11 is a titration curve for the reactivity of recombinant TbH-33 with sera from *M. tuberculosis* patients and from normal donors showing an increase in OD 450 with increasing concentration of antigen.

The reactivity of the recombinant antigens RDIF6, RDIF8 and RDIF10 (SEQ ID NOS: 184-187, respectively) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. RDIF6 detected 6 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; RDIF8 detected 14 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; and RDIF10 detected 4 out of 27 *M. tuberculosis* sera and 1 out of 15 normal sera. In addition, RDIF10 was found to detect 0 out of 5 sera from PPD-positive donors.

The antigens MO-1, MO-2, MO-4, MO-28 and MO-29 described above in Example 5, were expressed in *E. coli* and purified using a hexahistidine tag. The reactivity of these antigens with both *M. tuberculosis* positive and negative sera was examined by ELISA as described above. Titration curves showing the reactivity of MO-1, MO-2, MO-4, MO-28 and MO-29 at different solid phase coat levels when tested against four *M. tuberculosis* positive sera and four *M. tuberculosis* negative sera are shown in Figs. 12A-E, respectively. Three of the clones, MO-1, MO-2 and MO-29 were further tested on panels of HIV positive/tuberculosis (HIV/TB) positive and extrapulmonary sera. MO-1 detected 3/20 extrapulmonary and 2/38 HIV/TB sera. On the same sera groups, MO-2 detected 2/20 and 10/38, and MO-29 detected 2/20 and 8/38 sera. In combination these three clones would have detected 4/20 extrapulmonary sera and 16/38 HIV/TB sera. In addition, MO-1 detected 6/17 sera that had previously been shown only to react with *M. tuberculosis* lysate and not with either 38 kD or with other antigens of the subject invention.

EXAMPLE 10PREPARATION AND CHARACTERIZATION OF M. TUBERCULOSIS FUSION PROTEINS

A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was
5 prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 141 and 142), PDM-57 and
10 PDM-58 (SEQ ID NO: 143 and 144), and PDM-69 and PDM-60 (SEQ ID NO: 145-146), respectively. In each case, the DNA amplification was performed using 10 µl 10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at either 70 ng/µl (for TbRa3) or 50 ng/µl (for 38 kD and Tb38-1). For
15 TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for
20 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7^L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and then digested with EcoRI for direct cloning into the pT7^L2Ra3-1 vector which was digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7^L2Ra3/38kD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed to BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD₅₆₀ of 5 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times 10 with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

15 The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 147 and 148, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 151.

20 A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:145 and PDM-83 (SEQ ID NO: 200) being used for amplification of 25 the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DraI site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and 30 PDM-85 (SEQ ID NO: 201 and 202, respectively) and 1 µl DNA at 50 ng/µl.

- Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and cloned directly into the pET28Ra3/38kD/38-1A construct which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 203 and 204, respectively.
- A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.
- Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 343 and 344, respectively) and 2 µl DNA at 100 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min; and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sca I (New England Biolabs.) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing.
- Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 345 and 346, respectively.
- A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.
- 38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 347 and 348, respectively), and 1 µl PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec; and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and

then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7ΔL2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7ΔL2 construct was designed to have a 5 MHHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn II (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New 19 England Biolabs) and Eco RI. Ligations were done with a ligation kit from Panvera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared essentially as described above. The 15 DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 349 and 350, respectively.

EXAMPLE 11

USE OF *M. TUBERCULOSIS* FUSION PROTEINS FOR SERODIAGNOSIS OF TUBERCULOSIS

The effectiveness of the fusion protein TbRa3-38 kD-Tb38-1, prepared as described above, in the serodiagnosis of tuberculosis infection was examined by 25 ELISA.

The ELISA protocol was as described above in Example 6, with the fusion protein being coated at 200 ng/well. A panel of sera was chosen from a group of tuberculosis patients previously shown, either by ELISA or by western blot analysis, to react with each of the three antigens individually or in combination. Such a panel 30 enabled the dissection of the serological reactivity of the fusion protein to determine if

all three epitopes functioned with the fusion protein. As shown in Table 5, all four sera that reacted with TbRa3 only were detectable with the fusion protein. Three sera that reacted only with Tb38-1 were also detectable, as were two sera that reacted with 38 kD alone. The remaining 15 sera were all positive with the fusion protein based on a cut-off in the assay of mean negatives +3 standard deviations. This data demonstrates the functional activity of all three epitopes in the fusion protein.

10

TABLE 5
REACTIVITY OF TRI-PEPTIDE FUSION PROTEIN WITH SERA FROM *M. TUBERCULOSIS*
PATIENTS

Serum ID	Status	ELISA and/or Western Blot Reactivity with Individual proteins			Fusion Recombinant OD 450	Fusion Recombinant Status
		38kd	Tb38-1	TbRa3		
01B931-40	TB	-	-	+	0.413	+
01B931-41	TB	-	+	+	0.392	+
01B931-29	TB	+	-	+	2.217	+
01B931-109	TB	+	±	+	0.522	+
01B931-132	TB	+	+	-	0.937	+
5004	TB	±	-	±	1.098	+
15004	TB	-	+	-	2.077	+
39004	TB	-	+	-	1.675	+
68004	TB	+	+	+	2.388	+
99004	TB	-	+	±	0.607	+
107004	TB	-	-	±	0.667	+
92004	TB	-	±	±	1.070	+
97004	TB	+	-	±	1.152	-
118004	TB	-	-	±	2.694	+
173004	TB	+	+	+	3.258	+
175004	TB	+	-	+	2.514	+
274004	TB	-	-	+	3.220	+
276004	TB	-	+	-	2.991	+
282004	TB	+	+	-	0.824	+
289004	TB	-	-	-	0.848	-

308004	TB	-	+	-	3.338	+
314004	TB	-	+	-	1.362	+
317004	TB	+	-	-	0.763	+
312004	TB	-	-	+	1.079	+
D176	PPD	-	-	-	0.145	-
D162	PPD	-	-	-	0.073	-
D161	PPD	-	-	-	0.097	-
D27	PPD	-	-	-	0.082	-
A6-124	NORMAL	-	-	-	0.053	-
A6-125	NORMAL	-	-	-	0.087	-
A6-126	NORMAL	-	-	-	0.346	+
A6-127	NORMAL	-	-	-	0.064	-
A6-128	NORMAL	-	-	-	0.034	-
A6-129	NORMAL	-	-	-	0.037	-
A6-130	NORMAL	-	-	-	0.057	-
A6-131	NORMAL	-	-	-	0.054	-
A6-132	NORMAL	-	-	-	0.022	-
A6-133	NORMAL	-	-	-	0.147	-
A6-134	NORMAL	-	-	-	0.101	-
A6-135	NORMAL	-	-	-	0.066	-
A6-136	NORMAL	-	-	-	0.054	-
A6-137	NORMAL	-	-	-	0.063	-
A6-138	NORMAL	-	-	-	0.041	-
A6-139	NORMAL	-	-	-	0.103	-
A6-140	NORMAL	-	-	-	0.212	-
A6-141	NORMAL	-	-	-	0.056	-
A6-142	NORMAL	-	-	-	0.051	-

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 6) demonstrate that all four antigens function independently in the fusion protein.

TABLE 6
REACTIVITY OF TbF-2 FUSION PROTEIN WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa2	Tb38-1	DPEP
B931-40	TB	0.57	-	0.321	-	-	-	-	-
B931-41	TB	0.601	+	0.396	+	-	-	-	-
B931-109	TB	0.494	-	0.404	-	-	-	-	-
B931-132	TB	1.502	+	1.292	+	+	+	+	+
5004	TB	1.806	+	1.666	-	-	-	-	-
15004	TB	2.862	+	2.468	+	-	-	-	-
38004	TB	2.443	-	1.722	-	-	-	-	-
88004	TB	2.871	-	2.575	-	-	-	-	-
99004	TB	0.691	-	0.971	-	-	-	-	-
107004	TB	0.875	-	0.732	-	-	-	-	-
92004	TB	1.632	-	1.394	-	-	-	-	-
97004	TB	1.491	-	1.979	-	-	-	-	-
118004	TB	3.182	+	3.045	+	-	-	-	-
173004	TB	3.644	-	3.578	-	-	-	-	-
175004	TB	3.333	-	2.916	-	-	-	-	-
374004	TB	3.696	-	3.716	-	-	-	-	-
276004	TB	3.243	-	2.56	-	-	-	-	-
282004	TB	0.249	-	1.254	-	-	-	-	-
289004	TB	1.375	-	1.17	-	-	-	-	-
505004	TB	3.708	-	3.353	-	-	-	-	-
144004	TB	1.563	-	1.399	-	-	-	-	-
317004	TB	1.162	-	0.92	-	-	-	-	-
312004	TB	1.709	-	1.485	-	-	-	-	-
380004	TB	0.238	+	0.461	-	-	-	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
473004	TB	0.188	-	0.469	-	-	-	-	-
410004	TB	0.384	-	2.392	-	-	-	-	-
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.357	-	1.456	-	-	-	-	-
325004	TB	0.947	-	0.196	-	-	-	-	-
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.123	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.133	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.12	-	-	-	-	-
Cat-off		0.284		0.266					

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

CLAIMS

We claim:

1. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Vai-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
- (b) Ala-Vai-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 17);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gin-Xaa-Ala-Val (SEQ ID NO: 119);
- (f) Ala-Glu-Gly-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Vai-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Vai-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123); and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gin-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132), wherein Xaa may be any amino acid.

3. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. A recombinant expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.

8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.

9. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with one or more polypeptides according to any of claims 1-4; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

10. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

11. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said

sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS. 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

12. The method of any one of claims 9-11 wherein step (a) additionally comprises contacting the biological sample with a 38 kD *M. tuberculosis* antigen and step (b) additionally comprises detecting in the sample the presence of antibodies that bind to the 38 kD *M. tuberculosis* antigen.

13. The method of any one of claims 9-11 wherein the polypeptide(s) are bound to a solid support.

14. The method of claim 13 wherein the solid support comprises nitrocellulose, latex or a plastic material.

15. The method of any one of claims 9-11 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

16. The method of claim 15 wherein the biological sample is whole blood or serum.

17. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

18. The method of claim 17, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 5.

19. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

20. The method of claim 19, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

21. The method of claims 17 or 19 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

22. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

23. The method of claim 22 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

25. The method of claim 24 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

26. The method of claims 22 or 24 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

27. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1-4; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

28. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

29. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 233, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 233, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

30. The method of any one of claims 27-29 wherein the binding agent is a monoclonal antibody.

31. The method of any one of claims 27-29 wherein the binding agent is a polyclonal antibody.

32. A diagnostic kit comprising:

- (a) one or more polypeptides according to any of claims 1-4; and
- (b) a detection reagent.

33. A diagnostic kit comprising:

- (a) one or more polypeptides having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
- (b) a detection reagent.

34. A diagnostic kit comprising:

- (a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and
- (b) a detection reagent.

35. The kit of any one of claims 32-34 wherein the polypeptide(s) are immobilized on a solid support.

36. The kit of claim 35 wherein the solid support comprises nitrocellulose, latex or a plastic material.

37. The kit of any one of claims 32-34 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

38. The kit of claim 37 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

39. The kit of claim 37 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin, dye particles and colloidal particles.

40. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 5.

41. A diagnostic kit according to claim 40, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 5.

42. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

43. A diagnostic kit according to claim 42, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 5.

45. A kit according to claim 44, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

46. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

47. A kit according to claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

48. A monoclonal antibody that binds to a polypeptide according to any of claims 1-4.

49. A polyclonal antibody that binds to a polypeptide according to any of claims 1-4.

50. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

51. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6 (SEQ ID NO: 99).

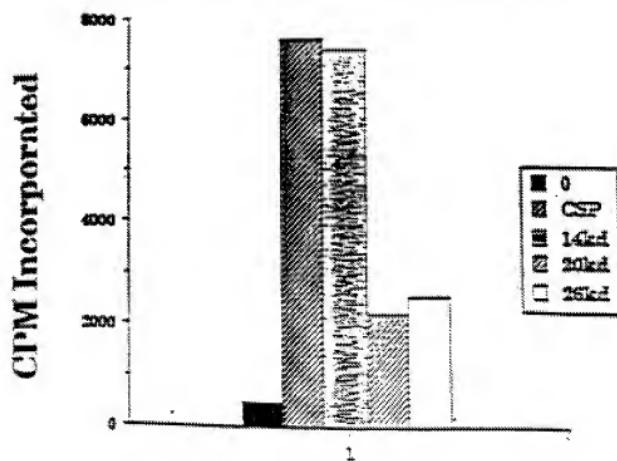
52. A fusion protein comprising a polypeptide having an N-terminal sequence selected from the group of sequences provided in SEQ ID NOS: 129 and 130.

53. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO: 150).

54. A diagnostic kit comprising:

- (a) one or more fusion proteins according to any one of claims 50-53; and
- (b) a detection reagent.

D7 T Cell Proliferation



D7 IFN_{fg}

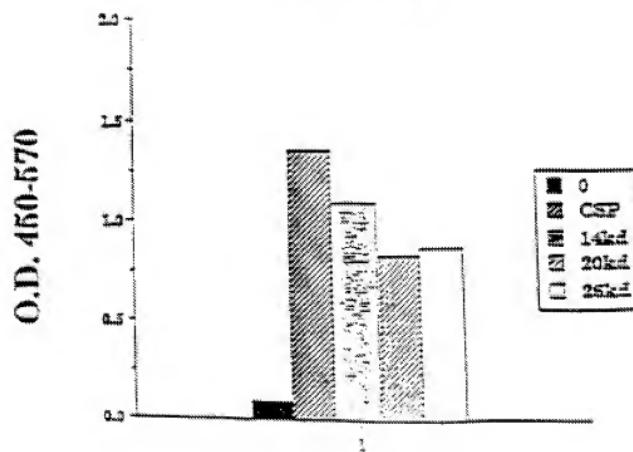
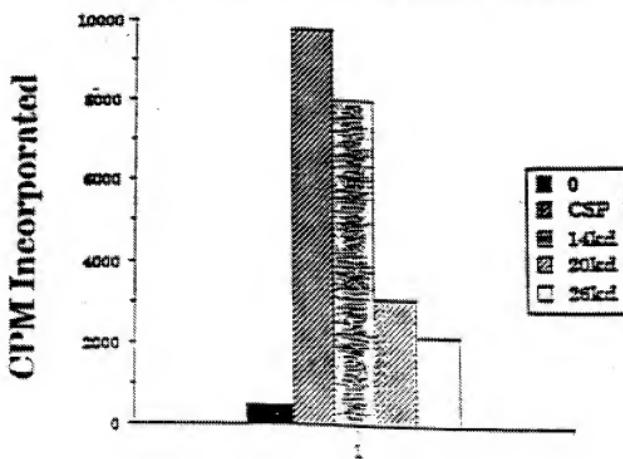


FIG. 14

D160 T Cell Proliferation



D160 IFN_α

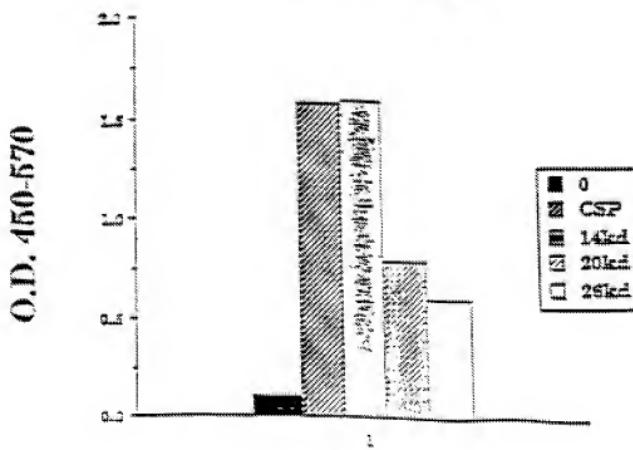
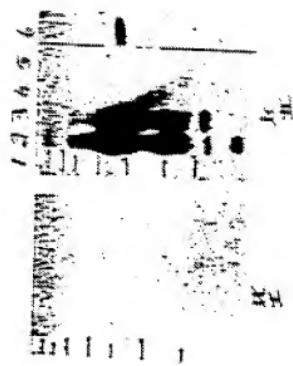


FIG. 1B

2A



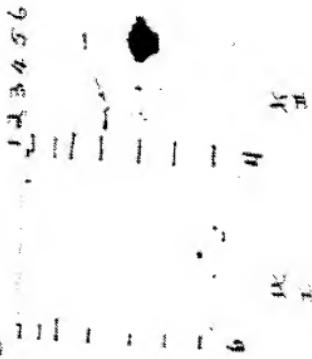
2B



2C



2D



FIGS. 2A-D

T cell clone 131TbH9 responds poorly to CSP

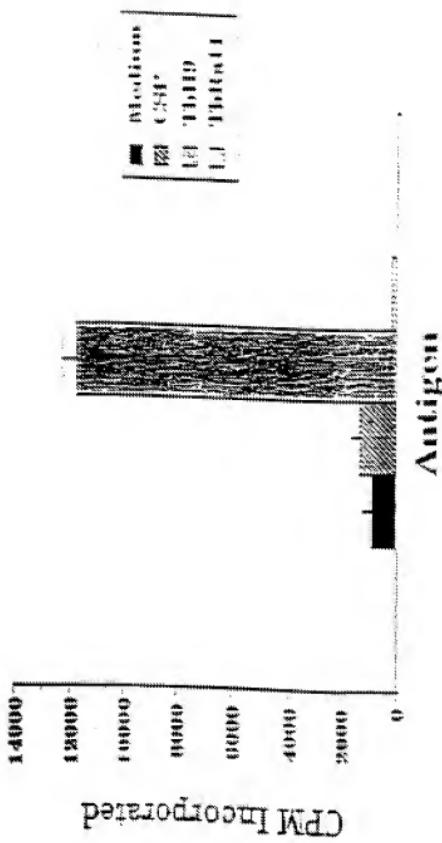
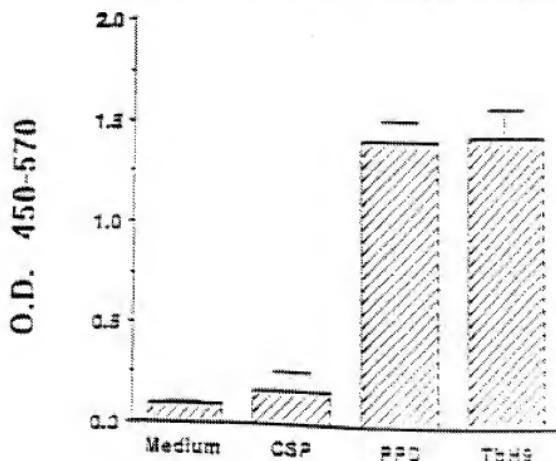


FIG. 34

T Cell Clone PPD 800-10 IFN γ Production**FIG. 3B**

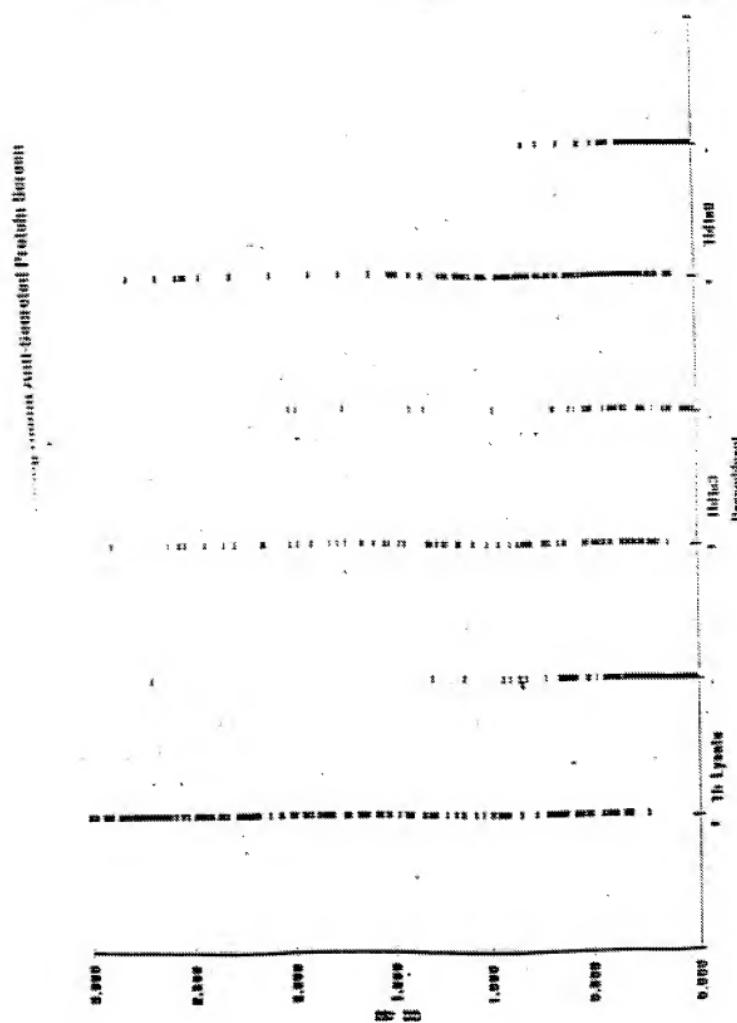
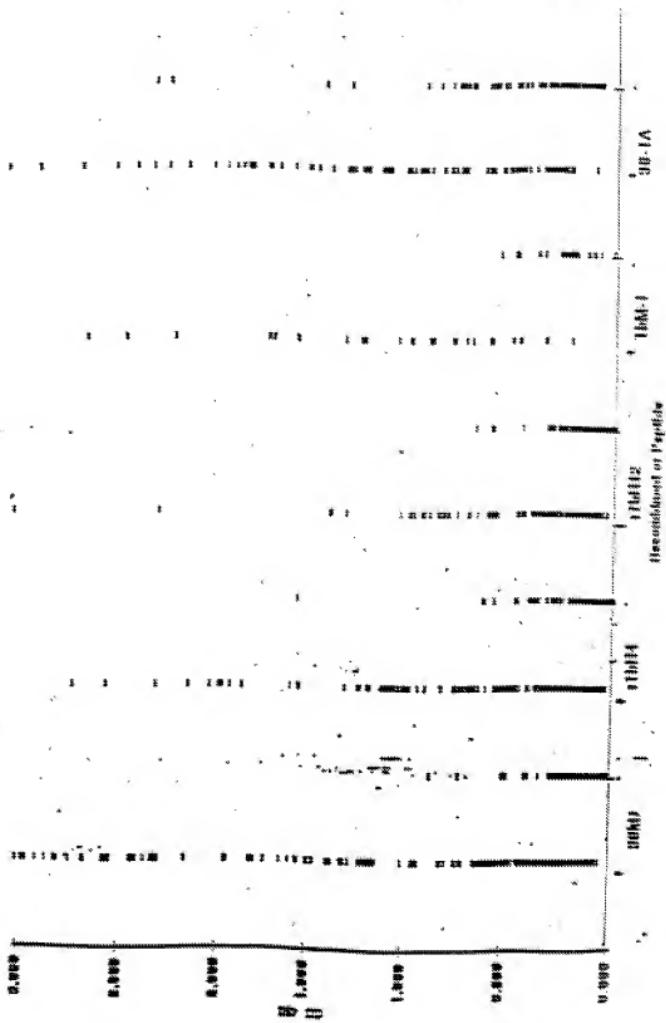
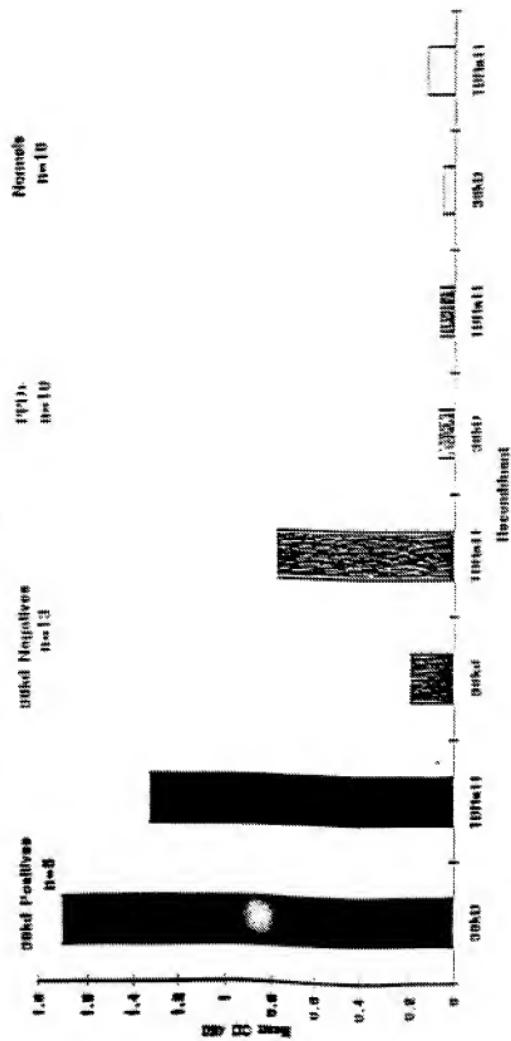


FIG. 4

**ELISA Reactivity of monoclonal and polyclonal antibodies against Human IgG1 from serotherapy
in patients**

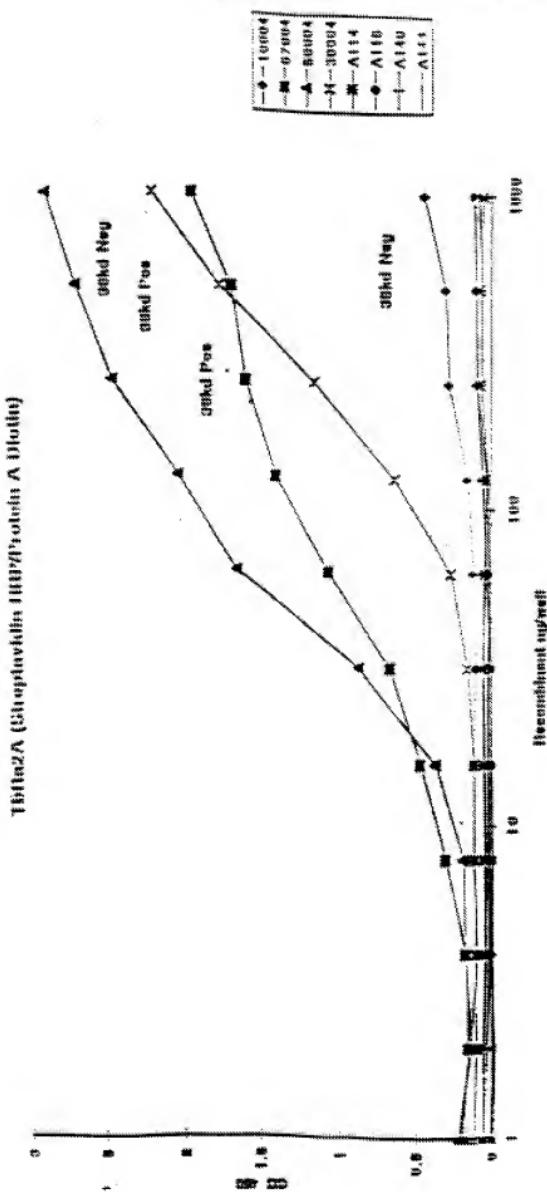




Sensitivity of Neomycinum (Mild) and VITAL I antibiotic with case from *A. tuberculos* patients.

6

7



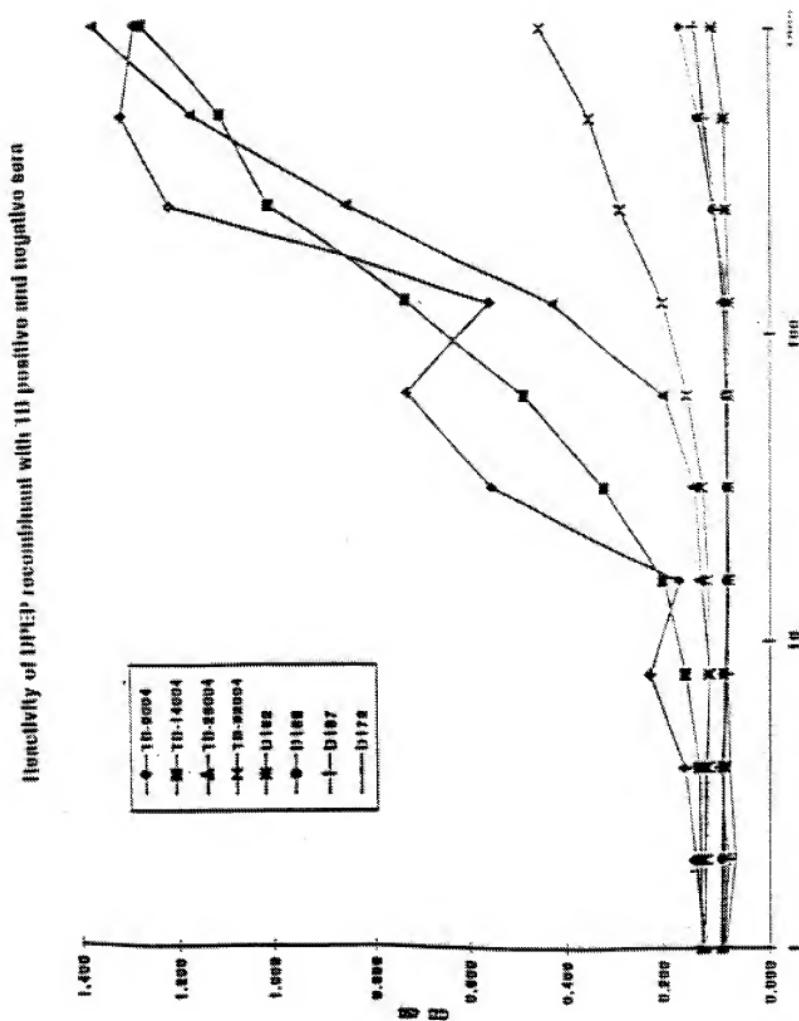
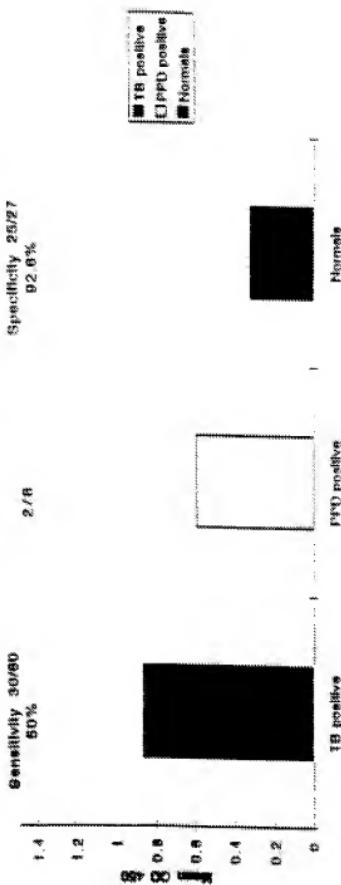


FIG. 9

TH1/29 ELISA reactivity in Streptavillin-1MIP/protein A-biotin system



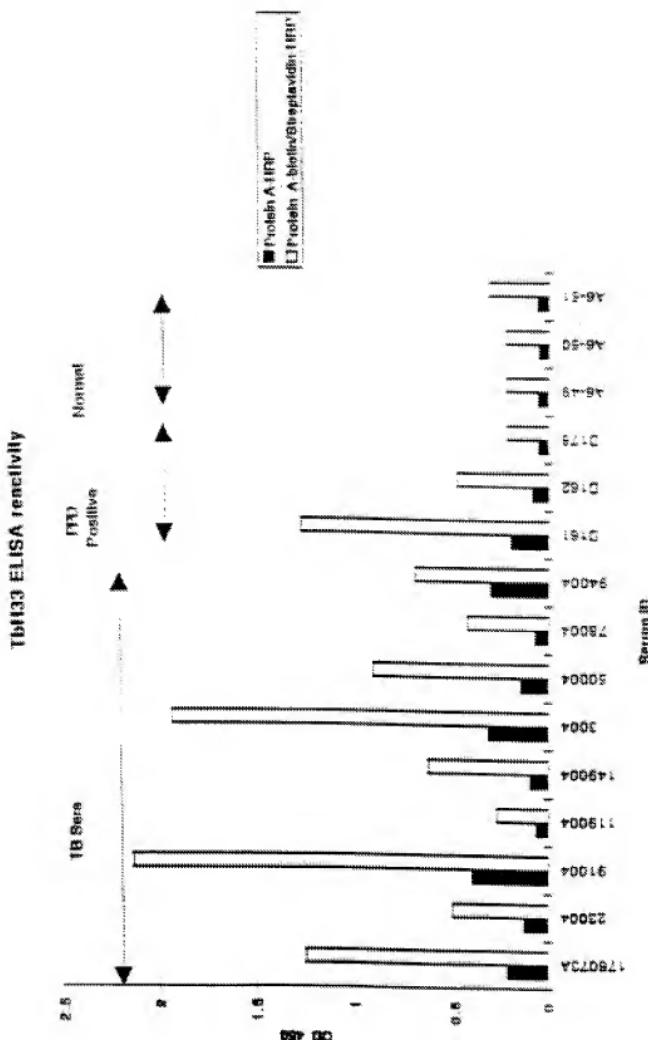
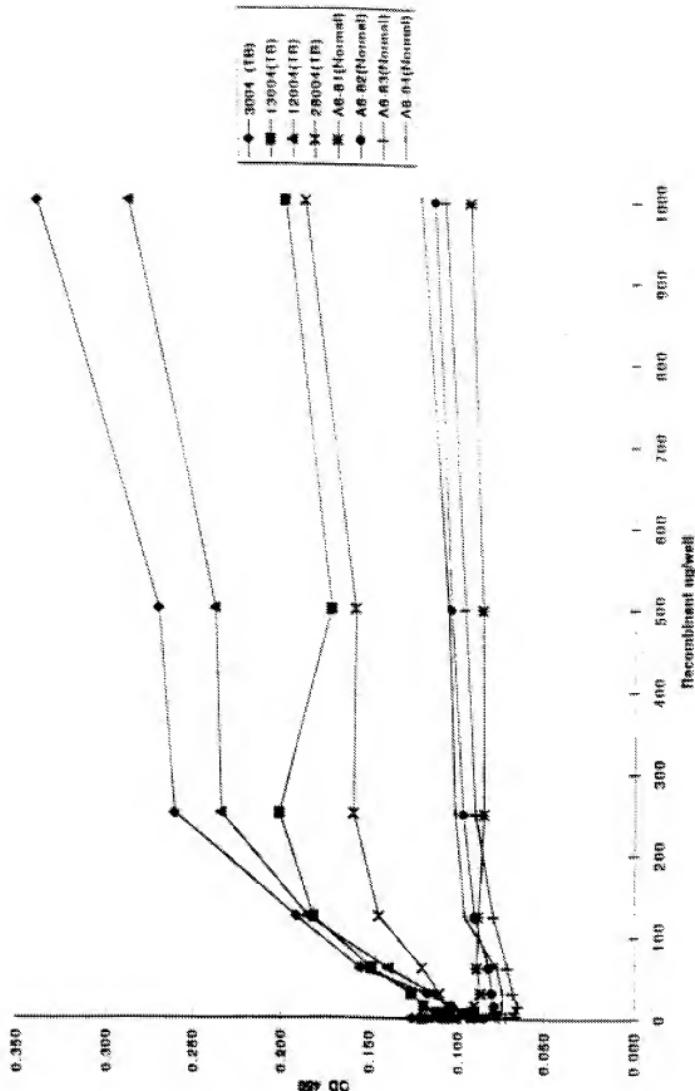
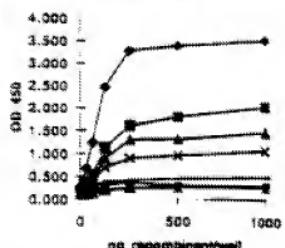


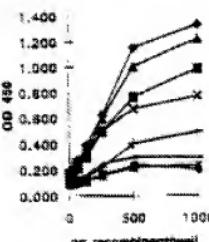
FIG. 10



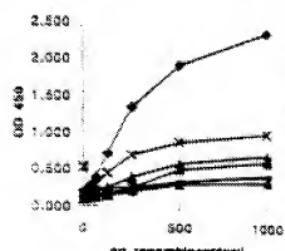
Titration of Mo-1 antigen with TB positive and negative sera



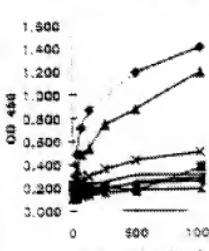
Titration of Mo-2 with TB positive and negative sera



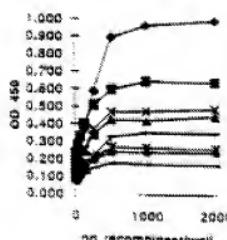
Titration of Mo-4 with TB positive and negative sera



Titration of Mo-28 with TB positive and negative sera



Titration of Mo-29 with TB positive and negative sera



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 390

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.10

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 05-MAY-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Makl, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.417CS

(ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAGGCCACG	GTAGTTTGA	CCAAACCGAC	AATGGACCGG	CAAACCAACG	GAAGAACACA	60
ACCATGAAAGA	TGTCGAAATC	GATGCCGCA	GGTCTGACCG	CCUGGGCTGC	AATCGCGCC	120
GGTGGGGCGG	GTGTGACTTC	GATCATGGT	GGCGGGCCGG	TGTTATACCA	GATCGACCG	180
GTGCTCTTCG	GGCGGCGACT	GGCGTGGAC	CGGGCATCGG	CCCTTGACGT	CCGGACCGCC	240
CCCCAGTTGA	CCAGCCTGCT	AAACAGCCTC	GGCGATCCA	ACGTGCGTT	TGCGAACAAAG	300
GGCGAGTCTG	TGAGGGGG	CATCGGGGG	ACCGAGCGC	GCATGGCGGA	CCACAAGCTG	360
AAAGAACCGG	CGAGACACGG	GGATCTGCCG	CTGTCTTCA	GGCTTGACGA	CATCGACCG	420
GGGGCGCCCG	GTTCGGCCAC	GGCGGACGTT	TGCTCTCGG	CTCCGAAGCT	CTCGTGGCG	480
GTCAACGCAAG	ACGTCACGTT	CTGTAATCAA	GGCGGGCTGGA	TGCTGTGAGG	GGCATGGGG	540
ATGGAACTTC	TGCAAGGGCC	AGGGAAACTG	ATTGGCGGGC	CGGTTTCAGC	CGCGCTGTTCA	600
GCTACCGCCC	CCGCGCTGGT	ACCGCTTCA	GTGAAACACT	GGCGGTGTA	GCACGGTGG	660
GTNTGGCGAG	GGCGCGACCG	ACCGGGCGGT	GCAAGCCCTC	CTGGAGATAG	GTGGTGTGTC	720
GGACGACAGG	ANACCCCCCN	NMTCGNCNWT	TCTCGNTGNT	GNATGA		766

(xii) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGUATCAC	ATCACCATCA	CGATGAACTC	ACCGTAGAGA	CGACCTGGGT	CTTCGGCGCA	60
GACTTCTCA	GGAGGCTGGA	CGCTCTCGG	AAAGCGGTA	CGAGAGCGC	GGTCTCCGGG	120
GTGGAGGGC	TCCCGCCGGG	CTCGGGCTTG	CTGGTAACTCA	AAAGAGGCC	CAACTCCGG	180
TCCCGGTTCC	TACTGACCA	ACCCATCACG	GGGGCTGGTC	GGCATCCCCA	CAGCGACATA	240
TTTGTGCGAC	ACGTGACCT	GAGCGCTGCG	CATGCTGAAT	TCCGGTTGGA	AAACACACAA	300
TTCAATGTCG	TGAGTGTGCG	GAATGTCACG	GGCACCTACG	TCAACCGGA	GGCGCTGGAT	360
TGGCGGCTGC	TGGCGAACCG	CGACGAGTC	CAGATGGCA	ACGTCGGTT	GGTGTCTTGTG	420
ACCGGACCCA	ACGAAGGCCA	CGATGACGG	AGTACCGGGG	GGCGCTGAGC	CCACCTGATA	480

GGCCCGCGCT GGCAGGGGATG TGGATGGGG CGGTCCCTCG ACCCTGCTACG ACCGGATTTC	540
CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTCAGGGTC NGGGTGACCC	560
CCCCCGGGC CTCATCTGGG GGNTNCGGCN GGTTCACCC CNTACCAACT GCNCAGGGN	580
TTGCAATTG TTCTCTCTGC GGCCHNAAG GGACCTTAN CTTCGGCTM GAJANGSTNA	720
TCGGGGCCC TTCTTGAAN CCCCTTCGCC CT	752

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCAACGATCACCA TCACACTCT AACCGCCAG CGCGTCGGG CGTCGAGCA	60
CCACGGCAAC CGGGCCCGA TCGATCTGT AGCTTGAGTC TGGTCAGGC TGGTCCTCAG	120
CAGCGCGATG CGCTATGTTT CTGCTCGACT CAGATATGCG GCGAAATCTAA TCTCCGGCT	180
GCGGCCGCGS GTGCTGCAA CTACTCCCG AGGAATTTCG ACUTGCGCAT CGAGATCTTC	240
ATGCTGGTCG CGGGTGTGTT TTGCTGCTGT TGGTCGCGTG TGGCTACAGC CGCGCGCAAG	300
ACCTACTGCG AGGAGTTGAA AGGCACGAT ACCGGCGAGG CGTGGCCAGAT TCAAATGTC	360
GACGCGCTT ACAACATCAA CATCGCGTG CGCGATTAACG ACCGGCAACTA GAGTCCTTG	420
GAARAAATTACA TGGCGCAGAC CGGGGACAAG TTGCTCAGCG CGGGCACATC GTCCACTGCA	480
CGCGAAGCCC CTGAGGATT GATATTCACG TGGCGCACAT ACCAGTCGG GATACCGGG	540
CGTGGTAAAGC AGGGCTTGTG GTCAGGGTC TACCAACG CGGGGGCGAC CGACCGAAC	600
ACCGCTTACA AGGGCTTGA ITGCGACCG CGCTTATCGCA AGCGAAATCAC CTATGACACG	660
CTGTGGCGGG CTGACACCGA TCGCTGCGCA GTGGCTTTCG CGATGTTGC AAGGTGAAC	720
GACGACCGA GACCGGGACA AGGGTATG ATAGCCGGCN AATGCCGCGT TGGAAACCCNG	780
TCAAATTATA ACAACTTCCG AGTACNAAA NAA	813

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAAC ACGGGCCGCGT CGGATAACTT CCAGCTGTTCG CAGGGTGGGC AGGGATTGCC	60
CATTCCGATC CGGCAGGGCA TGGCGATCGC GGGCCAGATO CGATGGGTG GGGGGTCACCC	120
CACCGTTCAT ATCGGGGCTTA CGGGCTTCTT CGGGCTTGCT GTTGTGCAACA ACRAACGGAA	180
CGGGCGACGA GTCCAAACCGG TGTCGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC	240
CGGGCACGTT ATCACCGCGG TCGACGGCGC TCGGATCAAC TC2GCCACCG CGATGGCGKA	300
CGGGCTTAAAC CGGGCATGTC CGGGCTGCT GTCTCTGGT GAACTGGCAAAC CGAAGTGGGG	360
CGGGCACGTT ACAGGGGAACG TGACATTUCC CGAGGGACCC CGGGCTTAT TTGCTGCGGG	420
ATACGACCCCC CGGGCCGGCC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGGCTACTGC GGTGGCGGAG TATGTCGCCC AGCGAAATTC TGCGAGCCGC CGAACGGAT	60
CGGGTGTATCC GAGGTTCCCGG TTTCATGAAAC CGGGCGCGCG GGAAGTATCG GTCCGATCTT	120
AGCCCCGGCGA CGGGGAGCGC CGAAATGGCC CGACTTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CGGGGGACGG NGAGCGCGCG AATGGCGCGA GTGAGGGAGGT GCGCAGCTAT GCGCAGNGTG	240
ATCGGAATCAA CCTGNATTCG GNCTGNGGN CCATTGACA ATCGGGATAC TGAGCGCAA	300
TGAAATGATG AAAACGGGNG GNGAGCTCCG ATGTTCTGGT GTGCTGTTAGGT GNCTGNCTGG	360
GGTGGNGGNT ATCGAGATAT TCTTCGCGA AACGTGATG CGAGGGAAACG GGTGTTNCGG	420
NNNNCCNAN GGNNTCCNAN CGCNNTTGT CGGNGGAAAT CGAAGAGNGG NTGAGNTNGT	480
NNAAAAGGTT GANCAGGNNN AAATNGGGN CCNAANAANC NNNNNNGNG NNAGNTNGT	540
NNNTNTNNNC NNRRNNNNNTG NNENGNCH NNNCAANCN NTNNNNNGUA NNCGNTNTTT	600
NAAT	634

(3) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCGACGCTCG AACCRCCTCA	CTAAAGGGAA CAAAAGCTTG AGCTCCACCG CGGTGGCGC	60
CGCTCTGAA CTAGTGTGATM TTTCGGGCTG CAGSAATYCG GVAAGGACAT TAGGACAGTC	120	
TAACGGTCTT GTTAGCGGTGA TCTAAATGACG GAGGACATTC TGTGATCGA CACCGAACAA	180	
CGGGTGCAGA CGCTCACCT CAACCGGCCG CAGTCCGYA ACGCGCTCTC GGCGGGCGTA	240	
CGGAGATCGT TTTCGGCGSY GTTGGYCGAC CGCGAGGYCG AGGAGGACAT CGACGCTGTC	300	
ATCTTCAACG GKGCGGATAC CGTGTCTTCG CGCGGACTGG ACCTCAAGGT AGCTGGCGCG	360	
CGAGACCGG CGTCCGGGACA TUTCACCGG WTGGGGGGCC ATGACCAAGC CGTGTGATCG	420	
EGCGATTCAT CGCGCCGGCG TCACCGGGCG GCTGQAACG TGCGTGTACT CGCGACATCT	480	
GATCGGCTTC GAGCAGCGCG CGTTTGGCGA CACCCACCGG CGGGTGGGGC TGTGCGCAC	540	
CTGGGGACTC AGTGTGTGCT TGTGCGAAA GGTGGGACATC GGTGCGGGC CGTGGATGAG	600	
CGTGAACCGGC GACTACCTCT CGTGACCGGA CCC	660	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGAGAC CGCGCGAGAG ASCCGGGCGC AACGGCGATC GACCCGGCCC TGGCCAGAGT	60
CGGCGACACT CAGGAGGAGG TGAATCATG AAATTNTCTA ACCNTATTGA CGCCCGTCCG	120
CGCCCGTGGAG CGGGCGGGCG CGTGGCGGAG GTCTATGCCG AGGCGGGCG CGAGTTGGC	180
CGCGCTGGCG AGCCGCTTCG CTGCTCTTCG CGGAGGAGG GACTGCTCAC CGCCGGCTGG	240
CGCGAGCTTCG CGGAGGAGCT CCTGCTGGCG CAGGTCGGCG GTGGCGGCAA GGAAGCGCTC	300
CGCGCGCGCG CGTGGCGGCG CGCTGCTGCG TGTACGCGACA CGACCGATG	360
CTGTACGCG CGGGCGAAC CGACGCTCC CGGGGGATGT TGCCCGGAC AGCACCTGCC	420
CGCGGGTACT CGAACCGGCCG CTATGTGGCG TGGGGGGCG GAAACCGGAC ACCGCGGGA	480

CGGGGGCAC CGTTCGCCCC GGATUTCGCC CGCGAATAACC TGGUCACCCC GGTGCAATTG	540
CACTTCATCG CACCGCTCTG CCTTGCTGCTG CTGGACGAAAGA CCTTCCTGCC CGGGGGCGCC	580
CGCGCCAC ACCTTCATCC CGCGCGCGGT GGAATGGTGT TGGCGCGCAA GTGCGCGCCTG	620
GAGCATCGGC CGGGCGCGTC CACCGCCCG CTGGAGCGGC GAACCGCTGCC CGACGATCTG	660
GCATGGCAA CACCGTCCA GCGCATAGCA ACCCGCTGCG CGCGCTCCAG CGACCAACTTG	700
GACACCGCC CGCACCTGCC GCCACCGACT CGTCAGGTTG TCAGGCGGCGT CGTGGGGTCC	740
TGGCACGGG AGCCAATCC GATGAGCAGT CGCTGGACGA ACGACACAC CGCGGAGCTG	780
CGCGCGACT TGACAGCGCT CGACCGTCTT CGCTCTGCA CGCGCTGCCG CGCGCATAG	820
GTGACCGACG CGACGUTGG CGGGGGCGCA TCGCTGCTCG ACACCGAGTC CGCGCTGCCGTT	860
CGCGCTGCCG CCTGGGGCG CGTCACCGCC CGCGGGCGCA TGGCACCTG GATGGCGCC	900
CGCGCCGAGG CGCAGGTTGC CGGGCAAAAC CGCGACTGGT GAGTGTGCC CGCGCTGCCG	940
TAGGGTGTCA TCGCTGGCTT GAGGGATCTC CGGGCGCGGA CGGGAGGTG CGACACAGGT	980
CGAACGTCG CGCGACTGGT TGGGGGGCGA CGCGCTGCCG CGCGCTGCCG TGGCGCGACT	1020
GGCGCGATCG UTGGGGCGCG CGCGCTGCCG GAAGGTCAG CGTAACTGTC CGTCACCGAA	1060
CGACCGACG CGTCACCGGG CGTCACCTGC CGCGCCAAAGG AA	1100

(i) INFORMATION FOR SEQ ID NO:8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCACTACCG CGATATGCCG CGCACCGTAG CGAAAGCGT CGCGACCGCA CTGGGGCGCC	60
CTATCGCTCC CGTGGAGGAC ATTCAAGGACT CGTGGAGGC CGCGCTGCCG CGAGCGCGTC	100
TGATGAACT CGCGCTGCCGTT TACATCACTT ACCGGCGAGG CGCGCCCCGAG CTGGGGACCG	140
CTAAAGCGTT CGTCGGCGTG CGGGACCGACT TAAAGCTGAG CTGGCGCGCC CTGACGGTAC	180
TGCGCGAGCG CTATCTGCTG CACCGACGAC CGCGCGCGCG CGCGGAATCG ACCGGCGAGC	220
TAATGAGCC ATCGGCGCGCG TTGTGTCGCG CGCGCGAGGA CGAATATGAG CGGGGCTGCG	260
CGAGGCGTGT CGCGCGCGCG TTGCGCGACCG TATTAACGAA CCTGGAAATTG CTGGCGAAATT	300
CGCGCGCTGT GATGAACTCT CGCACCGACG TGGGACTGCG CGCGCGCTGT TTTGGTTCTGC	340

CGATTGAGA TTTCGCTGCAA TGGATCCTTG CGACGCTGGG ACAGGGCCGC GAGCTGCAGC	540
GGGCTGAGG CGGCAACCGAA TATGCCCTCA GCGACCTGGC ACCCCCGGGG GATCGGGTGC	550
CCTCCACGGG CGGCRACGCC ACCGGGACCGG TGTGCTTGTAC AGCGCTGTAT GACAGTGGCG	560
CGGGTTGTTG CTCCATGGC GGTGCGCGGC GTGGGCGCTG TATGGCTGTC CTGGATGTGT	570
CGGACCGGA TATCTGTAT TTGCTCACCG CCAAGGCGGA ATCCCCCGAC GAGCTCCGG	580
ATTCGAACT ATCGGTTGGT GTGACCGAACG CCTTGGCTGG GGGCGTGGAA CGCAACCGCC	590
TACACCGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC CGGGATGCCG CGCCCGGAGC	600
TGTTGACSC CATGGCGAAA CGCGCGACG CGGGTGGCGA TCCGGGGCTG GTGTTTGTG	610
ACACGATCAA TAGGGCAAC CGGGTGGCGG GGAGAGGCCG CATGGAGGCC ACCAACGCT	620
CGGGGGAGGT CGCACTGGT CCTTACGAGT CATGTAATCT CGGCTCGATC AACCTGCGCC	630
GGATGCTGCG CGACGCTGGC STGACTGGG ACGGGCTCGA GGAGGTCGCC CGTGTGGCGG	640
TGCGGTTCT TGATGACGTC ATCGATGTCG CGCGCTACCC CTTCGGCGAA CTGGGTGAGG	650
CGGGCGCGCCG CACCGCGAAAG ATCGGGCTCG GAGTCATGGG TTGGCGGAA CTGCTTGGCC	660
CACTGGGTAT CGCGTACCGAC AGTGAAGAAG CGCTGCGGTT AGCCACCGGG CGCATGCGTC	670
GCATACAGCA CGCGCGCGAC ACCCGATCGC GGAGGCTGG CGAAGAGCG CGCGCATTC	680
CGCGCTTCAC CGATAGCTGG TTGGGGCGGT CGGGCGCGAG CGCGAACCGA CAGGTGACGT	690
CGCTGCGTCG CACGGGCGA	1458

(ii) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAAT CGTGCTGGAT CTGGAAACCGC GTGGGGCGCT ACCTACCGAG ATCTAATCGC	60
GGCGCAAGGG GCTGGGGCGT GGGCATCGCG TCCTGCTGAGT CGGGATCGCG GTGGCGATCG	120
TCATGGCGTT CGTCGACAGC AGGGCCCGGTC CGAAACCGGT CGGGCGCGAC AAAGGGCGCT	180
CGGGCCAGAG CGATCCCGGC CGCGGGCGAC CGCAAGGACCG CGGGCGCGCC GGGCAACCG	240
AAGGTAACGC CGCCGCGCGC CGGGCGCAAG CGCAAAACCC CGAGACACCC ACGGCCACCG	300

CCGCGGTGCA GCGCGCGCCG GTCGTCAGG AAGGGGACGA TTGCCCCUAT TCGAGGTGG
 CGCTCAAGG TTTGACCAAGC GCGCCUGAGT ACTACGTCGG CGACCAAGCG AGTTAACAA
 TGGTGTCAC CAACATCGGC CTGGTGTCT GTAAACCGGA CGTTCGGGCC CGGTGTTGG
 CGCGCTACGT TTACTCGCTG GACAACAAAGC GGTGGTGGTC GACCTGGAC TCGCGCGCT
 CGAATGAGAC GCGTGTCAAG AGCTTTCGCG CGGTGAGCA CGTAACGACG CGGTGACCT
 GGACCGGGAT CGGATCGCG CGCGCTCCG CATTGCGCG CGCGCGGATC GGGCGGGCA
 CCTACAACTT CGTGGTACAA CTGGGCAATC TGCGCTCGT GCGCGTTCG TCGATCTGA
 ATCAGGCGGC CGCGCGCCG GCGCTGGTAC CGCGCTCCGGG TCGAGCGACG CGCGCTCCGC
 CGGAGCTTCC CGCGCAAGGC CGATAATTAT TGATCGCTGA TGGTGGATTC CGCCAGCTGT
 GACAAACCGT CGGTGCTGCG CG
 360
 420
 480
 540
 600
 660
 720
 780
 840
 862

(i) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CGCGCAAGGC GTCACATGCC TCGCTGGGTG TCGAGGTGAC CGATGACAAA 60
 GACACCCCGG CGCGCCTAGAT CGTGGAACTA CTGGCGCGGTG CGCGTGGCG CGACGCTGG
 GTGCCGAAAG CGCTGTTGTG CACCGAGTCG GACGACCGCG CGATGACACG CGCGACGCG 120
 TTGGTGGCGG CGCTGCGCGTC CGAACGCCGG CGCGCCACAG CGTGGCTAAC CGTTCAGGAT 180
 CGCTCGGGCG CGAGCGCGAC AGTGCAGTC ACCTCGGGCA AGGCGGAGCA CGTGTGAAGG 240
 TGGCGCGCGA GTGTTCAAGG CTGGATATA CGTGGCGCAC CGTGAACAG CGTGGCGAGT 300
 TGGTGGTTGG CGCGGCACTT CTGCTCGTC TTGACGATCG CACGCGCAC CGCGATGAG 360
 ACCACAGCGG CGCGCTTGTG ACGGACGTCG CGACCGAGGC CGGGTTGGTT CGCGACCGCG 420
 TGGTGGCGGT CGCGGCGAC GAGGTGGAGA TCGGAAATCG GCTGAACACG CGCGTGTGCG 480
 CGGGGGTGGG CGTGGCTGGT TCGTGGCGCG CGACCGGCGTG GACGCGCTCG GATGTCAACC 540
 CGGAAGCCAC CGCGACGATT CT
 600
 660

(i) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCCAAGCGG	TAAGCTTGT	GGCGCCCGTC	ACACTGGTGT	TGACAGCATG	GGCGGTGCC	60
ACCAACAGCT	CCTCGTCAGG	CCGAGCGGA	ACGCTGCGGT	CGGTGCACTG	CGCGGGCAAG	120
AAGGAGCTCC	ACTCCACGGG	CTGACGCCA	CAAGAAATG	CCATGGAGCA	GTTCTCTTAT	180
GCCTACCTGC	GATGCTGCC	GGCTACACG	TTGGACTTACA	ACGCCAACGG	GTGGGGTCC	240
GGCGTGACCC	AGTTTCTTA	CAACGAAACC	ATTTCGCGG	GCTGGATGT	CCCGTTCAAT	300
CGCTGUACCG	GTCAACCTGA	CGGTCGCGG	CGCGGGTGC	GTTCGGGGC	ATGGGACGTC	360
CGACGGGTGT	CGGCCCCAT	CGCGATGCC	TACAATATCA	AGGGCTGAG	CACGGTGTAT	420
CTTGACGGAC	CCACTACCGC	CAAGATTTG	AAAGGCAACA	TCACCGTGTG	GAATUATCCA	480
CAATTCGAG	CGCTCAACTC	CGGACACGAC	CTGCCGCCAA	CACCGATTAG	GTTATCTTC	540
CGCGACGACA	AGTTCGGTAC	CTCGGACAAAC	TTCGAGAAAT	ACCTGGACGG	TATATCCAAC	600
GGGGCGTGGG	GCRAAAGGCG	CAGCGAAACG	TTCAAGGGGG	GCTGGGGGT	GGGGCCCGMC	660
GGAAACAACG	GAACSTCGGC	CCTACTCGAG	ACGACCGAGC	GGTCATCAC	CTACRACGAG	720
TGGTGTTCG	CGTGGGGTAA	GCAGTTCAAC	ATGGCCCAGA	TCATCACGTC	GGCGGGTGTG	780
GATCCAGTTC	CGATCACCC	CGAOTCGTC	CGTAAQACAA	TCGCGGGGC	CAAGATCATG	840
GGACRAGGCA	ACGACTTGGT	ATGGGACACG	TGTCGTTCT	ACAGACCCAC	CGAGCTGGC	900
TCTTCACCGA	TCTGCTGGC	GACCTATGAG	ATCGCTCTGT	CGAAATAACCC	GGATGCGACG	960
ACCGTACTG	CGTAAGGGCG	GTTCATGCAA	CGCGCGATTG	GTCCAGGCCA	ACGAGGGCTG	1020
CGACCAATACG	CGTCGATTCC	GTGCGGCAA	TGTTTCGAAG	CGAAATTGCG	GGCGGGGTGT	1080
AATGCTATTT	CTTGACCTG	TGAGGGAAAT	TGGACGGTGA	GGGATGGGT	TGGCAGGTA	1140
CGCTCGCAAT	TTGGGGCGTA	TCAGCTATTG	CGGCTGCTGG	GGCGGGCGG	GATGGGGCGAC	1200

(ii) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAACGAGCT	GCAGCTCGTC	CTTTGGACG	AACCTGGCAT	CCCGAAGACC	AAACGCCAAC	50
AGACCGCTTA	CACCGAGGT	CCCGACGGC	TGAGTCGTT	GTTCGACACG	ACCGGGUCATC	120
CGTTTCTGCA	ACATCTGCTC	CCCGACCGCG	ACGTCACCCG	GTCTCAGGTC	ACCGTCGACG	180
GTTTCTCTCA	AACGGTGGCC	CCCGACGGCC	GCATTCACAC	CACGTTAAC	CCAGACGATCG	240
CGCCGACGG	CGCGCTCTCC	TGACCGAAC	GTACCTGCA	GAACATCGC	ATCGCGACCG	300
ACCGGGCGCG	CGCGATCGG	GACCGCTTCG	TGTCGCGGGA	CGGTTACGCC	GAGTTGATGA	360
CGGCGACTA	CGACCGACG	GAGATCGGA	TCTGCGGCC	CCTGTCGCGG	CGCGAGGGCC	420
TCTATCGAGG	GTTCRACACG	GGGGAGGACT	TGTTATCGTT	CGTCGCGTC	CGGGTGTTCG	480
GTGTGCCCCAT	CGACCEAGTC	ACCGGGAGT	TGCGCGCGCG	GGTCRAGGCG	ATGTCCTACG	540
GGCTGGTTA	CGGGTGGACG	GCCTACGGCC	TGTCGAGGA	GTGRRAAATC	TCCACCGAAG	600
AAGCCRAAGA	CGAGATGAC	GGTTATTTCG	CCCGATTCGG	CGGGGGCGCC	GACTACCTTC	660
CGCGCTTACT	CGACCGGGCC	CCCAAGGACG	GTCTACACTTC	GAACGUTCTG	GGCGCGTCGC	720
GCTACCTCGC	CGAGCTGAC	AGCAACAAAC	GTCAACTCGG	GGAGGCGCGC	GGCGGGCGCG	780
CGCTGAAACG	CCGAGATCAC	GGCAGCGCGG	CCGACATCAT	CAAGCTGGCT	ATGATYLRGG	840
TGACACAGGC	GTCTAACCGA	GCACAGCTTG	GTCTCGCGAT	GTCTCTCAG	GTCCACCGACG	900
AGCTTCTTC	CGAAATCCG	CGCGTTCAG	GGGAGGGGCT	CGAGGCGCTG	GTGCGCGACG	960
AGATGGCGG	CGCTTACCGC	CTCGACGCTC	CGCTGGAGGT	GTGGGTGGCC	TACCGCGCGA	1020
GCTGGACCC	GGCGCGCGAC	TGAGTCGCGA	GGCTTCATCT	GGCGCGGGAA	TTGGCGGATT	1080
TTTCGCGCTT	GAATTCACCG	TGCGCGAT	CGGGACCGAG	TTTGTCGAGC	GTGTCACCGT	1140
CGCTAGCGCT	CGTCGA					1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGGCGCGTC	TGGTGTTCGA	ACGGTTTTAC	CGCTCGCGAT	CGGGACCGGGC	GTGGCGCGGT	50
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TCGGGGCTCG	GTTGGCGAT	CCTCAAAACAG	GTGGTGTCA	ACCACGGGG	ATTGCTGGC	120
ATCGAAGACA	CCGACCCAGG	CGGCCAGCCC	CCTGGAACCT	GTATTTACGT	GCTGCTCC	180
GGCGCTGGA	TGGCGATTC	GCAGCTTCCC	GGTGCGACGG	CTGGCGCTCG	GAGCGACGGAC	240
ATCGAGAACT	CTCGGGGTTG	GGCGAACCTT	ATCTCAGTGG	AATCTCAGTC	CACGCCGCGA	300
ACCTAGTTGT	GCAGTTACTG	TGAAAGCCA	CAACCATGCC	AGTGCACCGA	TGGCCAAGTT	360
GGCGGAGTA	GTGGGGCTAG	TACAGGAAGA	GCACCTAGAC	GACATGACGA	ATCACCCRCG	420
GTATGCCA	CCGGCGCNCG	ACCCCGGGAC	CCCAGGTAT	GCTCAGGGGC	AGCAGGAAAC	480
GTACAGCCG	CAGTGGACT	GGCGTTACCC	AGCGTCCCGG	CGCGCGAGC	GAACCGAGTA	540
CGCTCAACTC	TCAGGAGCGT	TGGCTGTAC	CGCGCCCGT	CTGATACCTG	GCGTGAATTG	600
GACCATGACG	CCCCCTCTTG	GGATGTTTG	CGAACCGCTT	CUTCGACGCA	TGTTGGCCAT	660
CGGCACGCGT	ACGATAGCGG	TGGTGTCCC	CGCGATGCC	GGCGCGCGCG	CATCCCTGGT	720
CGGTTCAAC	CGGGCACCGS	CGGGCCCCAG	CGCGGGCCCA	GTGGCTGCCA	GGCGCGCGCC	780
AAACATCCCC	GCACCAAACA	TGCGCCCGG	GTGGTGTGAA	CAGGTGGCG	CGAAGGTGCT	840
GGCCAGTGTG	GTCTATGTTGG	AAACCGATCT	GGGCACCGAC	TGGAGGAGG	GCTCGGGCAT	900
CATTGTGTT	GGCGAGGGGC	TGATTTGAC	CAACACCCAC	GTGATCGCGG	CGCGCGCCAA	960
GGCTCCCTG	GGCGATCGCG	CGCGAAAAC	GACGTTAACG	TTCTCTGACG	GGCGGACCGC	1020
ACCGTTGACG	GTGGTGGGGG	CTGACCCAC	CAGTGATATC	GGCGCGCTTC	GTGGTCAAGG	1080
CGTCTCTGGG	CTCACACCGGA	TCTCCCTGGG	TTCTCTCTGG	GACCTGAGGG	TGGTGAGCC	1140
GGTCTGGCC	ATGGGTTGCG	CGCTCGTTT	GGAGGCGACG	GTGACCGACG	GGATGCTCAG	1200
CGCTCTTAC	GTTCGAGTGT	CGACGACCGG	CGAGGCGCGG	AAACGAAACA	CGCTCTGGA	1260
CGCCATTGAG	ACGGACCGCG	CGATCAACCC	CGGTAACTTC	GGGGCGCGCG	TGGTGACAT	1320
GAACGCTAA	CTCTCGGAG	TCAACTCGGC	CATTGGCGAG	CTGGGCGCGG	ACTCGCTGA	1380
TGCGCAGAGG	GGCTCGATCG	GTCTCGTTT	TGGATTCGA	GTGGACCAAG	CGAAGCGCAT	1440
CGCCGACGAG	TTGATCGACG	CGGGCAAGGC	GTGACCATGG	TCCCTGGGTC	TGAGGTGAC	1500
CAATOACAAA	GACACCCCGG	CGSCCAAGAT	CGTGGAAAGT	GTGGGGGCTG	GTGCTUGCGC	1560
GAACGCTGGA	GTGCGGAAAGG	GGCTCGTTGT	CACCAAGGTG	GAGGACCGCC	CGATCAACAG	1620
CGCGGACCGG	TGGTTGCCG	CGCTGCGGTC	CAAGGCGCGG	GGCGCCACGG	TGGCGCTAAC	1680
CTTTCAGGAT	CGCTCGGGCG	GTAGCGCGAC	AGTCAACTC	ACCGCTGCCA	AGCGGGAGCA	1740

GTGATGAAGG TCGCCGGCGCA GTTTCAAAG C

1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGCCACCGCG	GTGCGCGCG	CTTGTAGACT	AGTGGATCCC	CCGGCGTGCA	GGAAATTGGC	60
ACGGAGGATCC	GACCTTGCG	GTGTCGAC	CCCCCGCGC	GGAACTATCG	GTCCATGCC	120
AGCCCGGCGA	CGGGCGAGCG	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGCGC	180
CCGGCGACCG	CGAGCGCGG	AATGGCGCGA	GTGAGGGAGGC	GGGCACTCAT	GGCCAGCGTG	240
ATCCAACTCA	CCTGCATCG	GGCTCGCGC	CCATTGACA	ATCGAGGATAG	TGAGCGCAA	300
TGAATZGATG	AAAACCGCG	GTGACSTCG	CTTGTCTGT	GGTGTCTAGG	GCCTGCGCTGG	360
CGTTGTGGCT	ATCAGNATGT	TCTTGCGGA	AACCTGATGC	CGAGGAACAG	GGTGTTCGCC	420
TGAGCGCGAC	GGCTCGCG	CCCCCGCTCG	TCGGCGAGAT	CGGGCACTCG	CTTGATCGA	480
CAAAAGGTT	CGCCAGCGT	CGCTGAGCG	TCGGAAACLA	GGGGAAAGTC	GACNGCTTC	540
TGGTATTAC	CACTGGCGAT	GTGACCTCG	GGGCAATCG	GCTCGCGGC	AAGGGCGTAT	600
CGACTTACRA	CGAGGAGCG	GGTGTCCCGT	TTCGGGTACA	AGGGACACAC	ATTTCHGTGA	660
AACTGTTGCA	CGACTGGAGC	AACTCTGGCT	GGATTTCTGA	ACTGTCAACT	TCACCGCTGC	720
TGGATCTG	CGCTGGGTG	ACCGACCTCG	TGTGGGTGT	CGGAACCTC	CGAGCGCAAG	780
GTACCGAGT	GTAGACCGA	ATTCGACCGA	CGAAAATCAC	CGGGACCGTC	CGGGCGAGGT	840
CTTGTAAAGAT	CGTGTACCT	GGGCGCAAGA	GTGCAAGGCT	GGCGACCTTG	TGATTTGCGT	900
AGGACGGCTC	CGACCACTC	GTCCGAGCG	CGATGACCT	GGGATCGGG	TGATTTCAGC	960
TCACGCACTC	GAATGGAAC	GAACCGCTCA	ACCTGGACTA	GGCGGAAGTT	GTCTGACCG	1020
GTGTGTGCAA	ACGGCGTTT	GAACGGGTTC	AAACGNA			1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCCGCA	CGAAGAGGTGA	TGACATCAT	CGGGACCGGC	CCCACATCCT	GGGAACAGGC	60
GCCCCCGGGAG	GGGGTCAGC	GGCGCGGGGA	TAGGCTCGAT	GACATCCCGC	TGGCTCGGGT	120
CATTGAGCG	GACATGGCGC	TGGACAGGCG	CGGCAAGAGTC	ACCTACCGCA	TCAAGCTGAA	180
ACTCTCTTTC	AAGATGAGGC	CUGCCAAACC	GGGCTAGCAC	GGGGCGGCAG	GCAAGACGCA	240
AAATCCACG	GTTCGCGTT	GATTCGTCG	AITTTTGTCG	TGCTCGCCGA	GGCTTACCGAG	300
GCCTCGGCCA	GGTCCGCGT	GGGGCTTATC	CAGGGTGCAG	TGCGGATTCG	GGGGCCACG	360
CCGGAGTTAA	TGCTTCGGT	CGACCCGAAAC	TGGGGATCC	GGGGGNGAGC	TGATGGATGA	420
CCCTGGCG	CCCTCGAT	CCCGATTCG	CGAGGAAAC	GTGCTTCCAG	GGGGTAGGA	480
ACGTCCTGTA	GGCGCGGCGT	CTGACCGGCT	CTGCTCGCC	CTTCAGTCAG	GGCAAGCGAGC	540
33						542

(ii) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCTGCGGCC	GGGGCTCCG	TTGGCCCGAT	TGCGGCGTC	GGGGATCAGC	TGCGCATCGC	50
CACCATCAAC	GGCTTTCGCG	CCGGCACCGC	GGGTGGCGC	GGGGCGCGCG	ATGCCACCGC	120
TTGACCTTGG	GGGGCGCGCG	GGGGATTCG	ATACACGAGC	GGGGCGCGCG	GGGGTTAC	180
GGCTGCGCA	GGCTGCGCG	GGCTTACCTT	TGAGGCCGG	GGGGCGGAAT	GAACCGCGCG	240
CAAGCCCGCG	GGGGCACCG	TTGGCCCGCT	TTCCCGCGCG	GGGGCGCGCG	GGGGCAATTG	300
GGGAACAGCC	AMGCAACGTT	GGGGCACCG	GGGGCGCGCG	TAACCGGCT	GGGGGGCGCG	360
GGGGCGCGCG	GGGGCGTTAC	GGGGCGTTAC	GGGGCGTTAC	GGGGCGCGCG	GGGGGGCGCG	420
TTTTGGCGC	AAATATCGGC	GGGCACCGCC	AGACCCCGCG	GGGGCACCAT	TGCGGCGCGG	480
CACCGAAACA	ACAGGCGAAC	GGTGGCGCG	GGGGCGCGCG	TGGCGCCAT	CACCGGGCGAT	540
TCACGGCGAG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	600
GGGGCGCGCG	GAGNGCGTC	GGGGCGCGCG	GGGGCGCGCG	CAAAGCGCG	GGGGCGCGCG	660

CGGCCCCCGCC	GGACCCACCG	GTCCCCCGGA	TCCCCCGTT	GGCCCGGGTC	GGGGCGCAT	720
TGCTCTCT	GAAGCGTTA	GCGCGGTTTC	CACCGGTTCC	GGCGTGGCG	CCNTGGCGC	780
CGGCCCCCGCC	GTTCGCGTAC	AGCCACCCCG	CGGTCGGCCC	GTTCGGCGCA	TTGGCGGCAT	840
TGCCCGCGT	GGCCCGATTC	CCGGCGTTCC	GGCGCGCCAC	GGCGGTTGG	CCGGCGGCAC	900
CGGGCGCGGC	CGC					913

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTT	GTGTAGAAAA	ATCTCTCCGC	CCGGACCCCT	AAGGCTUGGA	CAATTCTGAA	60
TAGCTACCC	GACACAGGAG	GTTAACGGAT	GAGCAATTGG	CCGGCGCGCT	CACTCGAGTC	120
GTCTATGTT	CTGAGCGTGC	TGGCTAACUT	CGGGCTGGGC	CTGGCCACGG	GGCCCGCCCA	180
GGGGGGCGG	CGGGCGCTGT	CGCAAGGACCG	GTTCGGCGAC	TTCCCGCGCG	TGCCCGCTGA	240
CGCGTCCCG	ATGGTCGCCCC	AAGTGGCGCC	ACAGGTGGTC	AACTCAACG	CCAAACCTGG	300
CTACAAACAC	GGCGTGGCGG	GGGGGACCGG	CACTGTCATC	GATGCGACG	GTCTGTGCT	360
BACCRACAAAC	TACGTTTACG	CGGACCGCAC	CGACATTAAT	GGTTTACGGC	TGGGCTCGG	420
CGAAACCTAC	GGCGTGGATG	TGGTGGGTTA	TAACCGGACT	CAGGATGTC	CGCTGTGCA	480
GCTTGCGCGT	GGCGTGGGGG	TGGCTCTGGC	GGCGATCGGT	GGGGCGCTCG	CGGTTGCTGA	540
GGCGTGGTC	CGCGATGGCA	ACAGCGGTGG	CGAGGCGCGA	ACGGCCCGTC	CGCTGCGCTGG	600
CAGGCGTGGTC	GGCGTGGGGC	AAACCGTGGCA	CGCGTGGGAT	TGGCTGACCG	GTGCGGAGA	660
BACATTGAAAC	GGCGTGGATCC	AGTTGGATGG	CGCAATCGCG	CCGGGTGATT	CGGGCGGGCC	720
CGCTGTCRAC	GGCGTGGGAC	AGGTGGTGG	TATGACACG	GGCGCGTGG	ATAACTTCGA	780
CGCTGTCRAC	GGTGGGCGGG	GATTGGCGAT	TGGCGATCGG	CGGGCGATGG	CGATGCGGG	840
CGAAATCCGA	TGGGTTGGGG	GGTCACCGAC	TGGTCAATATC	GGGGCTACCG	CGTTCGCGG	900
CTTGCGGTGTT	GTGCGACAACA	ACCGCGAACCG	CGACACGACTC	CAACCGCGTGG	TGGGAAGGCC	960
TCCGGCGCGCA	AGTGTGCGCA	TGGCGACCGG	CGACCGTGCAC	ACCGCGGTGG	ACGGCGCTCC	1020

GATCAACTCG CCCACCCGGA TGGCGAGC GC GCTTAACGGG CATCATCCG GTGACGTAT
 CTGGTGAAC TGGCAAACCA AGTCGGCGG CACCGTACA GGGAACTGCA CATTGGCGA 1080
 GGGACCGCCCG GCGTGATTG TOGCCGATAC CACCGCGCGG CGGGCCATTG GGATTGGCGC
 CAGCCGTGAT TGCCCGTGA GCCCCCGAGT TCCGGTETCCC GTGCGCGTGG CATTGTGCAA 1140
 GCAATGAACG AGGCAGAACAA CAGCGTTGAG CACCGTCCCG TCGAGGGCAAG TTACGTCGA
 GCGCGTGGCG TCGAGACATCG GGATGCCAAG GACTTCGGCA GCGCGCGCGC CCTGGCGCGC
 GATCGGACCT GGTAAASCA CGCCGCTTTC TAGCGAGTGC TGTGCGGGG GTGCTTCGAC 1200
 CGCAGCGCGG ACGGTTCCG CGATCTGGT GGACTCATCG ATCGGCTCGA CTACCTSCAG
 TGGCGTGGCA TGGACTCTAT CGTTCGCGG GGTTCGTCAG ACTCACCGCT GCGCGACCGC
 GGTGAGACA TTGCGQACTT CTACAGGTT GTGCGCGAT TGGGCGACUT CGACGATTTC 1260
 GTGCGCGTGG TCGACACCGC TCACCGGGCA GGTATCGCGA TCATCACCGA CCTGGTGTAC
 AATCACACCT CGGAGTCGA CCCTGGTTT CAGGAGTCGG GCGCGACCC AGACCGACCG
 TAGGTTACT ATTACGTTG GAGCGACCC AGCGAGCGT AGACCGACGC CGGGATCATE 1320
 TTGGTGTACA CGGAGAGTCG GAAGCTGCA TTGGATGCTG TCGGGGACA GTTGTACTG
 GCAACGATTC TT 1380
 1381

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGGCGGAA ACCTGATGCC GAGGAACCGG GTGTTCCGCT GAGCCCGGAGC GGTGCGACG
 CGCGCTCTT CGCCGAGATC AGGCAGTCG TTGATGCCG AAAAGGCGTGC ACCACCGCTGC
 ACCTAGCGGT CGGACAAACC CGGAAACTG ACAGCTTGTG GGTGTTTACG AGTGGCGATG 60
 TGGACGTTG GCGCAATCG CTGGCGCGAA AGGGCGTATG CACCTACACG GACGAGCAGG
 GTGTCGCGTT TCGGGTACAA CGGACAAACG TCTCGTGGAA ACTGTTCCAC GACTGGAGCA 120
 ATCTCGCGTC GATTTCGAA CTGCGACTT CGCGCGTGT CGATCTGCG GCGGGGTTGA 180
 CGCAGCTCTT GTCCGCGTGT AGCAACCTCC AAACGCGAAAGG TACCGGAAGTG ATAGACCGAA
 TTGGGACAC CAAACGTCAC CGGACCGATC CGCGCGACTC TGTCAAGATG CTTGATGCTG 240
 241
 300
 360
 420
 480

GGCCCGAGAG	TGCAAGGCCG	GGACCGCTGT	GGATTGCCA	GGACGGCTCG	CACCGCTCG	540
TCGGAGCGAG	CATCGACCTT	GGATCCGGGT	GGATTCAGCT	CACCGCTCG	AAATGGAAACG	560
AACCGCTCAA	CCTCGACTAG	GGCGAAGTT	GGTGGACCGG	TTGGCTCGAA	GGCCCTTGTC	660
AAACGGTGTCA	ACCGCACCGC	AAACATGACC	CCCTGACGGC	ATCTGAAAAT	TGACCCCTTA	720
GACTGGCGG	TTCGGTGTAA	TTCTTCGTTG	GTTCGGCTCT	GTGGGACCGG	GGCGAGGTGC	780
GGGTCTTGTG	GGCGGTAGCT	GTGCGCTTTC	ARGGGGACGA	CTTCAGCATG	GTGGACCGGG	840
CGGTGATCA	TGGGGCGCGC	AAACGCTCG	GGCGGCGCGA	AAACCTGCCC	CCACGGCGCG	900
AAAGGCTTAT	TOGACUTTCG	GATGAGCTG	GGCGCGCTCA	ACCGGGAGGA	CACCAAGCTCG	960
AAAGAAGAGT	GGCGGGCTTC	GGGGTCAAC	GGATATSTAC	GGACTTCGTC	AACCRCCCGG	1020
ACCGGATAGC	GGCCAACCG	GGTGAGTTG	GGTAGAGATTC	GGCGGGCTCG	GTGAGCTCG	1080
GGCGAACGTC	CTACCCATTG	GGCGGCGTGT	GGGAACACCGA	CCCGATGACT	GGCGTGACAC	1140
GGCGGTATCG	GGAGGGCGAC	GGGAAGATGA	GTCTTCCCGG	GGCCAGGCAG	GGCCCCAAAAAA	1200
CACTACCTTA	TGGGGCGCGG	TGATGAAATC	GGGGGTGCCC	AGATGTGCGA	TGGTGTGCG	1260
TTTGAGCGA	GGAGCAATCT	CAAGTGGAA	GTCTTCCGAA	GGGGGAGCG	GGGGGAGCG	1320
GGCGGGCGG	ATCGGGCGCT	CAACCGCTG	GGACTCCCGG	GGTGACACTT	GGGGCTCGAG	1380
GGAGGGCGCG	AGGATATTCT	GGGGGTGCA	GTGCGCTCG	GGGGCGCGAT	GGGGCGCG	1440
GGACACTGAC	TCACCGAGGG	GGGGAGCTT	CAATGCTCTT	GT		1480

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTGCCA	GGAGGGCGG	ATAGCTTCTG	GGCGGGCGCC	GGCCGAGATGG	CTGGAGGTTT	60
GGTGTCTCGG	GGCAGGGCGG	GGGGCACCCAC	CCTGACCGGT	GAGGCGCTTC	AAACGGCGGA	120
GGGTGACTCG	TTGGTGTCTG	ACGGCAACCA	GGGGGGCGTG	GTGGCGTACG	ACCCGGCGTT	180
GGCGCTACAA	ATCGGGCTACA	TCTGGGAAAG	GGGACTGGCC	AGGATGTGG	GGGAGAACCC	240
GGAGAAACATG	TTCTTCTACA	TCACCGCTCA	GGACGAGGCC	TACGTGCGG	GGGGGGCGCT	300

GGAGAACTTC GATCCCGAGG	GGGTGCTGGG	GGGTATCTAC CGTTATCAGS CGGCCACCGA	360
GCAACGCACG	AACAGAGGCC AGATCTGGC	CTCCGGGGTA GCGATGCCCG CUGCGCTGCG	420
GGCACACAG	ATGCTGGCGG	CCGAGTGGGA TGTGGCGCC GACGTGTGGT CGGTGACCG	480
TTGGGGCGAG	CTAAACCGCG	ACGGGGTGGT CATGGAGACC GAGAAGCTCC GCACACCGA	540
TGGGCCCGCG	GGCGTGGCGT	ACGTGACGAG AGCGCTGGAG AATGCTGGG GCGCGGTGAT	600
CGCGGTGGCG	GACTGGATGC	GCCTGGCTCCC CGAACGAGATC CGACCGTGGG TGCGCGGCG	660
ATACCTCACG	TTGGGCACCG	ACGGGGTCCG TTTTCCGAC ACTCGGGCGG CGCGTGGCG	720
TTACTTCAAC	ACCGGGCGCG	AATCCCGGGT TGGTCGGGGT TTTGGGAGGG TTGGCCCGCG	780
TGGACGGGTT	AATATCCACC	CATCGGGTGC CGGTGCTGGG CGCGCGCGCC AGTTACCGCG	840
ATTGACGCAA	GGTGGGGGGT	TGGCGCCGAA TAAGTT	876

(ii) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG	GCTGCAAGAA	TTCCGCRGCA GAGACRAAAT TCCACGCGTT AATGCAAGAA	60
CAGATTCA	ACGAAATTTCG	ACGGGCAACAA CAATATTCG CGATCGGGT TTATTCGAC	120
ACCGAAGACC	TGCGCGCTTG	GGCGAAGCAT TTTTACAGCC AAGCGGTGCA CGAACGAAAC	180
CATGCAATGA	TGCTCTGCGA	ACACCTCTTC GACCGGJACG TTCTGTGCGA AATTCCCGCG	240
UTAGACACGG	TGGAAAACCA	TTGCGACAGA CGCGCGAGG CACTCGCGCT GGCGCTCGAT	300
CAGGAACGCA	CAGTCACCGA	CCAGGCGGT CGGCTGACAG CGCTGGCTCG CGACGAGCG	360
CATTTCTCG	CGGAGGAGTT	CATCGAGTGG TTCTTGCAGG AACRGRGCGA AGAGGTGGCC	420
TTGATGGCAA	CCCTGGTGC	GGTTGCGCGAT CGGGGGGGGG CGAACCTTTT CGAGCTAGAG	480
AACTTCTCG	CACGTCAGT	CGGCGGGCGT CAGGCGCCCG GCACGCTGCC	540
GGGGGGCGCC	TCTAGATGCC	TGGGGGGGGAT CAGCGAGTGG TCCCGTTGCG CGCGCGCTCT	600
TCCAGGCCGG	CGTCTGCGC	GGCGGGGCGTGG TGAGTACCAA TCCAGGCCAC CGCGCGCTCG	660
CGGNAAAAGT	CGATGTCCTC	GTACTCATCG ACGTTCCAGG AGTACACCGC CGGGCGCTGA	720
CGTCCCGAGC	GGTCACGCGA	TTCGCGATAT TCTTTAACG CAGGCACTGAA CGTCTCCAGC	780

GGGTTGGCC CGACCGCCGT GGCAGCACTG CTGGTCAGGT ATCGGGGGGT CTGGGGAGC	840
AACRAACCTCG GCAGGAGGGG TGGACCCCGC CGGATCCCA GACCGGGGGC GCGAAACGA	900
CATCAACACT GCACGGGATC GATCTGGGA GGGGGTGGC GGAATACCGA ACCGGTGTAG	960
GAGCGCCAGC AGTTTTTTT CCACCAGCGA AGCTTTTCG GTCATGGG CGCNNTTAAG	1020
T	1021

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTGCCACG AAGGAAAGA CACAAACCTG AAGATGTTTC AATGGATGGC CGCAGGCTCG	60
ACCGCCCGGG CTGCAATTGG CGCGCTGGG CGCGGTGTA CTTCGATCAT CGCTGGCGN	120
CGCGCTGTAT ACCAGATGCA CGCGGTGTC TTGGGGGGC CACTGGCGT CGAACCGGNA	180
TGGGGCGTGG ANGGCGGAG CGCGCGCGAG TGGACCGAGC TGTCAACAG NGTCGNCAT	240
CCGACGCTGT CGTTTGNGAA CAAGGONAGT CTGGTCGAGG GGCGNATCG NGGNANCGG	300
GGNNONONATC GNCRANCA A	321

(3) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGGTTGGC GACGGGTTTT GGGGGCGGGT GTTAAACCGC CTGGGGAGC	60
CGATCAACCG CGCGGAAACG CTGGACTCG ATACTCGGCG CGCGCTGGAG CTGGAGGGCG	120
CCTGGGTGGT GNACCGGCAA CGCGTGAAGG AGCCGTTTGA GACCGGGATC AAGGGGATTS	180
ACCGGGATGAC CGCGATGGC CGGGGGCAGC CGCGGTGAT GATGGGGAC CGCAAGACCG	240
GCGAAACCG CGTGTGTGT CGGACACCAT CCTCAAACCA CGGGAAAGAA CTGGGAGTCC	300
GGTGGATCCC AGAAGGAGG TGGCTTGTG TATACGTTGG CGATGGGGCA AGAAGGGAA	360

CTTACCATCG CCG

373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCAT GATGGGATTG CTGGGCAGGG CGGGTCCTCT GCCTGGTGTC GATCAAGAAC	50
TGTTTACCCG GGTGCCGCAA GGCTGGTGTG TTGCTCAGGC AGCCGCTGTC CGGTGGTGT	120
TCTTGACCGC CTGGTACCGG TTGGGGGATT TAGCCGAGAT CAAGGGGGGC GAATCCTGTC	180
TGATCCATGC CGGTACCGGC GGTTGGGCA TGGGGCTTGTGAGCTGGGT CGCCAGTGGG	240
GGCTGGAGGT TTTCGTCAGT CCCAGGCGTG GAAACTGGGA CACGCTGGGC CGCATTCNGT	300
TTGACCGAGGA NCATATCGG NGATTCCNC ACATTCGAAG TTCCGANGGA GA	353

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCCGG TTCACTGGT TCGACCAGCG GCTGGCGATA ATCGACGGAA TGATCAAGCC	50
GGGGTTCGGG GCGCTCATGG GTCAACGGCA GAAATCGGCA AGTTCTCTGG TATATCGCAC	120
CTAGCGTCCA GTTGGCTGGC AGATCGCTT CGTACGGCTCA TGGCATGTAC CGTTGGCGT	180
CGCCACGCT CAGCTGGCG GCGTCACTCG TGCCCCACGGG TUTGGCGGGT CTGGGGGTCG	240
GGCGCGAGTC CGCAAGCCAA ACCGGCGGGG TGCCCCACTA CTACTGTCG CGGGGGCAGC	300
CTTTGACCC CGCATGGGG CGCAACTGGG ATCCCTACAC CTGGCATGAC GACTTCCACC	360
GGCAACAGCG CGGCCCCCGAC CACAGCCCGG ACTACCCCGG ACCGATCTC GAGGTTCCCG	420
TGCTTGACGA TCCCCTGCT GCGGGCGCGC CGCGCGCTGC CGGTGGGGGC CGATAGCGCT	480
CGGCGCATCG CGAATACCGG TATAAACCGG GCGCTGGCCC CGGCAAGCTA CGACTCCCG	540
CGGGGGCAGAT TTAGGCTTCG GTGGCGATGG ATGGCGCCGT CGGATGACAG	600
AAAATAGCGG ACCGTTTGGG GAAACCGCTG GAGGACGCTT GAAAGGGAACT TGTCTGAAAC	660

GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CGCGCACACCC CGTTCGCGGG	720
ATCGTGA	726

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACAGCG ACAGAACCTCG CGCGCACACCG CGCTTATCGC TTGATCGAGG CGACCGGGAT	60
CGTTCGCGAC CATATCCAG CAGCTCGGGT GCGCACTCGAG CGACCTTTTG ACCAGCCGGG	120
CTGCGCGATG CGCGGCCCGGT GAGCTCATTC CGCCCGGGGT TGTGCACCTG ATGAAACCGA	180
ATAGGGAACA ATAGGGGGGT GATTGGCGAG TTCAATGTCG GGTATGGCTG GAATCCAAAT	240
GGCGGGGCAT GTCGGCGGC GACCAAGCTG CGCGAGGGCG CGCAGCCCCG ATCTGGAGGG	300
AGCACTAAAT GGCGGCGATG AAAGCCCCGGA CGCGCGACCG TCCTTTGGAA GCAACTAAAG	360
AGGGGGCGCG AGTTTGATG CGACTACACG TTGAUGCTG CGTGTGCGCTG GTCTCGAGC	420
TGACACCCGA CGAACCGCGC GCACTGGGT AGCAACTCAA AGGCCTTAAT AGCTRAGACC	480
AGCGCAACCG CGAATGTCG CGTTCACCG CGACACCTTC CGTAGATGTCG CAGTGTCTCG	540
TCGGCGATGT ATGCCGAGGA GAACTTTCGG ATACAGCCTCT	580

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGGAGCG CGCGGGGGTTT TGCGGGGGCC CGGGCGCGCTCG CGCGCAACCG CGGGGGCGGCC	60
GCTACCGCCG GGTTCGTTGGG TGTGCGCGCG CGCGCGTGGG CGCGAGGCCA CGCGCATCGCC	120
GCTGTCAACG CTACGTCGGG CGACACACCG CGTGGATCCG	160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACGATA CGATGGTGAT GTACGCCAAC TTGTTCUACA CCTCGAGGC GTTCACCGATC	68
CAGCCGACAC CGACCGGGT GACCATCGGC GATGGGGCCC CTTCGCGGA GCGCGCTGCC	120
AAGGGATGG GAATCCAACT GCTGGGGTA ATTCCATACG GAATGGACCG GATCGTGCT	186
GAACCTGAAAC ACTGGGACGA CGGAAACAAAC ACGGTGGGCT TGGCGCCCG TGTGTTTC	240
CCCTACAGAGC GCAAGCTACAGACCGCC CG	272

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

- GCAAGCGGTC GTTCTGGAC TATCTGGCA CGTGTGACCGA GCGCGACCTG CGCGAGCTGA	68
ACCGGATGCA CGACAGGGAT CGCTTGCGGC GGTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACTGTGCCG GAGCGCGGCC GGTTCATCGG GGTGGACCGG CGGACGATCC	186
GTTCGGATCT GGCGTGTTG CAGACGCGCT ATTCGGTACG TGCGCTGCCG GCGTGGCTCC	240
GGATCTGAC CGCGAAGATC AAGAAGGGT CAAAGATCCA CGTCGTCAC AGTGGGTTCCG	300
CGGCGTGTGTT CGCGCGG	317

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATCA ACACCGTTGC CGAACCGCGCG GCGGGCAGCA CCTCGGTGTA	60
CGACGCGCGG ACCACCTGCC CGGTGGGAG CATTGCTGATG ACCACGTCGG CCTGGGCCAC	126
CGCTTGGGC CGCTTACGAA ACACCGCGAC ACCGTCGGCG GCGCGCGCG ACGCGCGCGT	180
CG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATGGCGAAG	TTCGGTGAAG	AGGTGGTCTGA	CGCGAAAATC	TGGGCCTCTG	CGAAGCCGCT	69
CGGCGTTAAC	GAGGCAGAAGA	CACGCCCTTC	CGAGCTCTTG	CGGCTCGTCT	ACGGCGGGCA	120
GGAGTTGAGA	TTCCCCCGCC	CGCGCACCGC	GTAGCAAAGC	TTCGGCGCT	GCATCTCTTG	180
GAGACTCTGC	CGTTAGGGAT	TGACCATGGC	GTGTACCGCG	TGCCCGACAA	TTTGGACGCT	240
CGGTTGTCAG	ACGACCTGCT	CGAACGCTTT	CACCGGTGAA	CGCGTACTTC	ATGGACACCC	300
ACGTTTGG						308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACACGCGA	JCAACTGCGC	TGGATGTTGG	TGGCGAGCGG	CATTGAGGCC	GGAGAGGATA	60
CGCCCGAAGC	TUCCCGCGGC	CAACTGCTCA	TAGTGACTGG	CGTAGAGCGG	CTGCCCGAT	120
GGCACCGGAC	TATTCTGGT	TGCCCTGGC	CGGTAACAGC	GGGTTAAAGA	ATGTGAGGGG	180
ACACGATGAG	CAATCACACG	TACCGAGTGA	TGGAGATCCT	CGGAGCTCG	CCGACACCGC	240
TGGACCGCGC	AATCCAGGGC	GGTGTGG				267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGGTCCCGA	AAGAATGTA	GGGUACACCA	TGAGCAATCA	CACCTACCGA	GTGATCCAGA	60
CTGGTCCCGAC	CTGGGCGGAC	GGCTCTGACG	CGGCAATCCA	GGGGGCTCTG	GGCGGAGCTG	120

CGCAGACCAT GCGGCGCGCTG GACTGGTTGC AAGTACAGTC AATTCGAGGC CACCTGGTGC	188
ACGGAGCGGT CGCGCACITC CAGGTGACTA TGAAAGTCGG CTTCGGCTGG AGGATTCCTG	240
AACCTTCAG CGCGCGCGAT AACTGAGGTC CATCATTAAG CGACTTTCAG AGAACATCTT	300
GAACCGCTCG AAACCGCGTT CAACCGACGG TGCGCTCCUCG GAACCGCTTC CTCCMAATC	360
CCTGCCGACAA TTCTGGGGCGG GCGCGCTACAA CGAACGGTGGT SCTGAAATTG TOGGGTATCT	420
GCTGGACCTG TGTGGGGTGC AGCGCGGAGA AGCGCGTCTC GACUTGGCT GCCTGCTCGG	480
GGGGATGGCG TTGCGCGTCA CGCGCTATCT GAACAGCGAG GGACGCTACG CGCGCTTGA	540
TATCTCGAG AAAGCGCATCG CGTGGTCCCA CGAACGACATC ACCTCGCGCC ACCCGAACCTT	600
CGAAGTGGAG GTCTTCCGACA TCTACAACTC GCTGTACAAAC CGGAAAGCGA AAATCCACTC	660
ACTAGACTTT CGCTTTCCAT ATCCCGATGC GTCGTTGGAT GTGGTGTTC TTACCTGGT	720
GTTCACCCAC ATTTTCCC CGGACGGTGG ACGTCTATCG GACCGAGATC CGCGCGTCT	780
GAAGCCGGC GGACGATGCC TGTGACGTA CTTCCTGCTC AATGACGAGT CGTTAGCGCA	840
CATGCGGAA CGAAAGAGTG CGCACAACTT CGACCATGAG GGACCGCGTT ATUGGACAT	900
CGACAGAAG CGCCCCGAG AAGCAATCGG CTTCGGGAG ACCTTCGTCG CGGATGTCTA	960
TGGCAACTTC CGCTTCCGCC TGCACGAAAC ATTGCACTAC CGCTCATCGA GTGGCGGGGA	1020
ACCACCGCTA AGCTTTCAGG ACATCGTCAT CGCGACCAAA ACGCGAGCT AGGTGGCGAT	1080
CGGGAAAGCA TCGCGACACT GTGGCGCGGA CGCGCGCTGC CGCGAGGCC ATTAGCGCGG	1140
CAGATTAAGCC CGCGCGCGGT CGCGCGCTGC ACTACCGCGC CGCGAATGCG GTCAACCGCT	1200
GGTAACCGAG CTTCGCGCGCT TGGCGCGCGG CTTCGCGCGAT CAGGTGGTAG ATUCCGACAA	1260
AGCGTCTG ATCGGTCTTC ACCACCGCTG ACAGCGAGCG GTTGCGCTCT AGGGCGAACG	1320
CGACCGCGGT CTCCGGGTCT GTCCAGCGGA TCGAGCGCGC CAAGCCCAAC TGACCAAAC	1380
CGGGCATCAC GTTGGCCGATC GGCGTACCGT GATAGCUAG ATCGAAATTT AAGGGCGCCA	1440
ATAGACTTCG ATCGCGCGAGA ACTTGGCGCTC GTTGGCGGT CGCGCGCTG ACCAGCTCC	1500
CGCGACGAGAA CGCGTACCGG TCGATCTCGC CTCTGTGCG	1519

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGGGCTG	GCCTGGATTA	GCTTCACCCG	GCGGCCAGGCC	GAAGCTGACCG	CCGGCCCAAGGT	50
CGGGGGTCT	CGGGGGGCCCT	ACGAGACGCC	GTATGGCTG	ACGCTGCCCC	CGCCGGTGTAT	100
CGCCGAAAC	CCTGCTGAAC	TGATGATTT	GATAGCGACC	AACCTTGGC	GGCAAAACAC	150
CCCGGGGATC	GCCTGCAACG	AGGCCGAATA	CGCGGAGATG	TGGGCCCAAG	ACGCCCCTGTC	200
GATTTTGCG	TACGCCCGCG	CAACCGAAC	GGCGACCGCG	ACGTTGCTGC	CGTTGCGAGGA	250
GGCCCGGGAG	ATGACCAACCG	CGGGTGGCT	CCTCGAGGAG	GGCCCGCGGG	TGAGGGAGGC	300
CTCGGACAC	GCCTGGGGGA	ACCGTTGAT	GTACATGATG	CCCCAGGGCC	TGAAACATT	350
GGCCGAGCC	ACUCAGGGGA	CAACGCTTC	TTCCAGGCTG	GCTGGCCCTG	GGARGACGTT	400
CTCGGCGAT	CGGTGCGGA	TCACCAACAT	GCTGTCGATG	GCCAACAACT	ACATGTCGAT	450
GACCAACTG	GCTGTTGCGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAAG	GCTTTGCTCC	500
GGCGGGGGCC	GGCGAGGCC	TGCAACCCG	GGCGCAAAC	GGGGTCCCGG	CGATGAGCTC	550
GCTGGGGAGC	TCTCTGGGT	CTTCGGTCTT	GGCGGTGG	GTGGCCCGCA	ACTTGGCTCG	600
GGGGGCTCG	GTACGGTATG	CTCACCGGGA	TGGGGAAAAA	TATGCAAGT	CTGGTCGGCG	650
GAACGGTGT	GGGGGTAAAG	GTTCACCCCG	GTTCGCTGGA	TGCGGTGAAC	TTGGTCACCG	700
GAACAGCTTA	C					750

(D) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATGGATCGG	GGCGGAATTG	GGACCGATT	CGCGTCGGC	GATACCCAA	TCAATGAAAC	40
CTAGATTTAT	TCCGTCGAGG	GGCCCGAGTA	ATGGCTCCA	GGAGAGGGAC	CTTACTGCTG	90
CGCGACACTG	TCTTAGGTCC	TOGATACCGC	GGAAAGGGCTC	GACATTTTCC	ACCGACGACCC	140
CCATCTAAAC	CTTGGAGGGC	CACTCCAGCT	TGTGAGGAG	GGGACCCAGT	CGCAGGCTGC	190
CGTTGGTCAA	GATC					240

(D) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATGCTGACC	GAAGCGGCCG	CGCCCAAGGC	GAAGTCGCTG	TTCGACCAAGG	AGGGACCGGA	60
CGATCTGGCG	CTTCGGATCG	CGGTTCAGCC	GGGGGGTGTG	GCTGGATTTC	GCTATAACCT	120
TITCTCTGAC	GACCGGACCG	TGGATGGTG	CCAAACCGCG	GAGTTGGTG	GTCGCAGGTT	180
GATGCTGGAC	CGGATGAGG	CGCGCTGTG	GGAAAGGCGCG	TCGATGCAIT	TCTTCGACMC	240
TATTGAGAAG	CGAGGTTAC	CATCGACAAT	CCAAACGCCA	CGGGCTCTG	CCGCTGGGGG	300
GATTGTTCA	ACTGATAAAA	CGCTACTAGC	ACCCCGCGGT	GGCAACACG	TACGGACCAA	360
CCAAGACCTG	ACCGCGCTGG	AAARGCAACT	GGGGATGCCC	TTCACCTGTA	CGCGGTGGCG	420
GGCGCGCGGC	GGCAGGTGTC	ACCTGCAATG	TGAACNGCAC	CTGGGCTGTA	TATTGCAACC	480
AGTACACGAT	TTTGTGCGATC	GGGGTCACTT	CGAACCTGGGA	GAACGCTTG	CGGAAACCGGT	540
GGCTGCTAG	CTTGGGCAAG	GGCTGATCGG	AGCGCTTTC	GGCGACGCCG	TCTGGTGTAC	600
CGCACAGCGG	ATTGCGAAACG	ATGGTGTCCA	CATCGCGGTT	CTCGACCGCG	TTGGAGGTATC	660
CCTGAATCGC	GGTTTGCGCC	GGTCCCTCCG	AGAAATGTCG	TGGCGTGTTC	GCTCGCGTGG	720
TGCGGACCCC	STATATGATT	GGCGCGCTCA	TAGCGACAC	CGCGCGACGG	GCTACCGAAC	780
TCCGATCG	CGACCGCTTG	TGGCGTGTG	GGGGTAGGGA	CACCTGCGGC	GGCACCGCCG	840
GATATGCGGC	GGGGCGACGG	GGCGCGCTGT	CTGCCGCGTC	GGGGGCGAAG	GGCGGTTGCG	900
GGGGCGCGAG	GTCTGCGGGG	TAGTCGAGG	CTTGGCGGTC	GTGGGATGAG	GCTCGCGGT	960
ACGGGCGCGG	TCGGTTGCGT	CGCACACCGG	GGTCCGGGCG	GTGGGGACCGT	GGCATTTGCG	1020
TTCTCTTAA	GTGGTGGACG	GGACCAACTG	CTAGGGCGAC	AACCGCCCGT	GGCGTCACCC	1080
GGCACACATG	CGAACATGGT	GGGCTCCCTA	GGCAGGCTAG	CGCAACACGT	GGCGTCACCT	1140
CTCAACCGCA	CGGGGGGGGG	CGCGCGCGCG	ATAATGTTGA	AAGACTAGCG	AACCTTAGGA	1200
ACGAAGGAGCG	GAGATTGTTG	TGCGGATC				1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGTGTCCG CGGATCGGCC GGGTGGTTGA ACGGCAACGG CGGGGGCGGC GGCCCCCGCG	60
GGACCGGGCGC TAACCGTGGT GCGCGCGGCCA ACGGCTGGTT GTTCGGGGCC GGCGGGTCCG	120
GGGGNGCCG CACCAATGGT GGNOTGGCG CGTCCGGCGG ATTTGTCTAC GCGAACGGCG	180
G	181

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTGTCCG CGGATCGGCC GGGTGGTTGA ACGGCAACGG CGGTGTGGC GCGCGGGCG	60
GGACCGCGCTT CTGGCGCGGT GCGCGCGGCC AGGGCGGGCT CGGTGGCCAG GCGCGCAATG	120
GGGCGCGCGTC CACCGCGGCC AACGGCGCTC TTGGCGGCAG GCGCGGTGGC GGAGGCAACG	180
GGGGGACCG CGGTTGGT GCGAACGGCG GAAAGGCTGG CGAAGGGCGN ATTGGCGCGCG	240
GGACTGAGAG GCGGACCGGGC CTGGCGGTG ACGGCGGTGA CGCGCGTGAC	290

(2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATTCAGCTG CATGCGGCT GTCACTUGAA GCAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTCTG CGTCGGCGGA TTGCCGGCGA CGCCACCGGT CCCACCGTTA CGCAACAGC	60
TGGCGTGGTC GCGACGACCG CGGGCACCGC CGACCGGGGA GTCGAACATA CGCACCGTGG	120
TATCCCCACC ATTGCCGGCG GNCCCCACCGG CACCG	156

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA CGGGGGCGCG CGGACCGGGC AGCCCGGNGG GGCCCGGGGG TCG	53
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(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCGACTGC CGGTGCGAGAC GGTGCGCGCG CGCCACCGC GACCGCGCGC CGCAACCGCG	60
CGACCGGGCG CAACCGCGCG AACCCGACCGC TGTGCGGGG CGCCCGGGGG CGCGCGCGCA	120
ACGGCGCGCAA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGCGCGC CGCGACCGGC CGCGACCGCG CGAAAGGGCG NAACCGGGGC CGCGAGCGCA	60
CGCGCGCGAGA ATUTCTCGCG TCCNCCAATG CGCGAAATGG CGGACAGGGC CGCAACGGCG	120
CGACCGGGCG GA	132

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 701 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGGCACGAGG ATCGGTACCC CGCGGCATCC GCAGCTGCCG ATTGGCGCGG TTTCGCCACT	60
CGAGGAAAGC CCTTACCCAGA TGGCGCTGCCG GAACTAGGGC GATCCGTTGC CGATGCCGCC	120
ATGAACCGGGC GGCATCAAAT TAGTGCGGGA ACCTTTCACT TTAGCCGACGA TAATGGCTAT	180
AGCCTAAGG AGGATGATCC GATATGAGGC AGTCCGAGAC CGTGACCGGTG GATCAACGAG	240
AGATTTGAA CAGGGCCRAAC GAGGTGGAGG CCCCGATGGC GGACCCACCG AGTGAIGTCG	300
CCATCACACC GTGCGAACTC ACGGGNGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG	360
CCGACAACAT CGCGGAATAAC CTGGCGCGCGG GTGCCRAAGA CGCGCGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGCGCGAAG CGTATGGCG AGGTTGATGA GGAGGCTGCG AGCGCGCTCG	480
ACACCGACGG CGAAGGAACT GTGCGGGCGA AATGGGCCGG GGCGCTGCGA CGGGACACTT	540
CGGCGAACT AACCGATACG CGGAGGGTGG CGACGGCCCG TGACCCRAAC TTCATGGATC	600
TCAAAGAACG CGCAAGGAGG CTCGAAACCG CGGACCTAAGG CGCATTTGCG CGCGACTGNC	660
GGGATGGGTG GAACACTING ACCCTGACCGC TGCAAGGCCG CG	702

(xii) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAACCCCGAG CGCTGTGCGG CGACGTGGCG CTCAAAGCGG CATCGCTCGG TGGCGCTGCG	60
GGCGCGCGGC TGCGCTGCCG CGCGGTGGGA TCGCGCGATCG CGGGCGCGGA ATCGGTGCG	120
CGCGCTTGGCG CTGGCTGACAT TGCGCGCTTA CGCGCGCGAA CGACCGCGCG CGGGCGCGCG	180
CTGGCGCGCG GTGGCGATGG AATCGCGATG CGTCCCGCGG ATCGAGGGACRA AGGGGGCGCG	240
AAGTCCGAGG GTTCTCGACG GGAAGACGAGG CGCGCTCTACA CGCGAGGATCC TCCTGCCG	296

(xii) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGCACGAGG ATCGATATCC GTCUCCGGGA GCACASCGTC GCACTGCCAC AGTGGAGGAG	68
CCATGACUTA CTGCGCGGGT AACCCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTCTAACG	120
GAGGCGTCAC ACCTCTGTTC GCGCAACGCCG ATGAGGGTGC GAGCAGCTTA CCGATGTACG	180
TGAACATCGC GGTGGCACTG CTGGGTCTGG CTGCGCTACTT CGCCAGCTTC GGCCCAATGT	240
TCACCCCTCG TACCGAACTC GGCGGGGGTG ATGGCGCAGT GTCCCGTAC ACTGGGGCTGC	300
CGGTGGGGT GGTCTGTG TGCTCGCTCG TTGGCGGGGT GGTCTGTG TGCTCGCTCG	360
AGACCCATGT GACGGTAGTT CGCGGTCTCG CGGTACTCGG GGTATTTGT ATGGCTCTCG	420
CGACCTTTAA CAAGCCCAACG GCTTATCGA CGCGTTGGGC ATGTTGGGTT GTTGGGCTT	480
TCATCGTGT CCAGGCCGTT CGCGCACTCG TGGCGCTCTT GGTGGAGACG GGCCTATCA	540
CCGGCGCGGC CGCCCGCGCCG AGTGGACACG CGTATGGACA GTACGGGCGG TACGGGCGT	600
ACGGGGCACTA CGGGGTGCGAG CGGGGTGGGT ACTACGGTCA GCAGGGTGTCT CAGCAGGCCG	660
CGGGACTCGA GTGGCGCGGC CGCGCACTCG CTGGCGCAGC TCCCGATAT GGGTCGCGAT	720
ACGGCGCGCTA TTGGTCCAGT CGGAGCCAT CGGGCACTCG ATACACTGCT CAGCCCGCG	780
CGTACGGGCGG CGCGCACTCG CGGTGCGACG AATGGCAACG CGCGCCATCC AGCCCGACCA	840
CGGGCTTTCG GAGCTTCAGC CGACCAACG CGGTCACTCG CGGGACGGCG TCCCGACCTG	900
GTTCGGCTCG AGTCAACTAT TCAAACCCCA CGGGGGGGCGA GCACTCTCG TCCCGCGGGG	960
GGGGCGGGGT TAAACGGGCG GTTCCCGCT CGGGTCGCGCG TGTGCGCGCA AGAGTAAACR	1020
GGGTGTCAGC AAACCGCGGAC GATCGCTGGT CGGAATTG	1088

(ii) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGGACGAGA GACCGATGCC GCTACCGCTG CGCAGGGAGC AGGTAATTC GACCGGGATCT	68
CGGGCGACCT GAAAACCCAG ATCGACCGAGG TGGAGTUGAC GCGAGGTTCG TTGCAAGGCC	120

AGTGGCGCGG CGCGGGCGGG AGGGCCGCCG AGGCCCGCGGT GGTGCCTTC TAAAGAAGCAG	180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCGGGCGTCC	140
AATACTCGAG GCGCGACGAG GAGCGACGAGC AGGGCGCTGTC CTCGCAAATG GGCTTGTGAC	160
CCGCTTAATAC GAAAAGAAC GGAGCAA	327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTGGCGAT GATGGCGTTG TCGAACCTGA CGGATTGTTGT ACCGCCGTCG TTGAGATCAA	60
CTAACAACTG GTTGGCGTGC GCAAATGTC CGAACCGCTG GATCTCGGTC ATCTTGTCT	120
TCTTCATCGA GAACTGCACA CGGGCGACCC TGCCCTCGGN TACCTTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCGGGCGG CACGGGGGGT GCCCGCGGCA GCAACGCTGG CGCTGGCGGC AACGGCGGGG	60
CGCGGGGGTG CGCGCGAACG GGTGGGTTGC TCTTCGGCAA CGCGCGCTGC GCGGGGCACG	120
GGGGCTGT	177

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGGCGGCAAG GCGGGCACCG CGGGCAACGG GAGGGGGCGG GCGGGGGCA AGGGCGGCAA	60
CGGGCGCTGC GCGCTAACG G	81

(2) INFORMATION FOR SEQ ID NO:50:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCAGGCTCC GGCAGAAAGC GCGGTAACCGC AGGAGACTGCC CGATGTTC	60
GCACAGGGCG GGCAGGNGGT GCGGGCGCT CCAACCAAGC CGGTAACCGC GGAGCCGGCG	120
GAACCGGTGG TCCCCGTGGG CTGATCTGG	149

(12) INFORMATION FOR SEQ ID NO:51:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGCCACGAGA TCACACCTAC CGAGTGATCG AGATGTCGCG GACCTCGCCC GACGCTCTCC	60
ACGGGNAAT CGAGGGCGGT CTGGCCCGAG CTGGCGAGAC CATCGCGCGG CTGGACTCTG	120
TGAACTACA GTCAATTGGA GGCACACTUG TGACCGAGAC GGTGGCGCAC TTCCAGGTGA	180
CTATGAAAGT CGGCTTCGCG CTGGAGGATT CCTGAAACCTT CAAGCCCGCG CGATAACTGAA	240
GTTGCTTCTT TAAGGCACTT TTCCAGGACA TGTGACCGCG CTGGAAACCGC GTTGTGCGCG	300
ACGGTGGCTC CGCCGAGGCG CTGGCTCCAA AATCCCTCGC ACGATTCGTC GCGCG	355

(13) INFORMATION FOR SEQ ID NO:52:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCTCA CATGCTTCAG GTGGACCCCA ACTTGACACCG TGGCAAGGGAA	60
CGATTGGCGG CACTGGCTAT CGGGGGCATG CGCAGCGCCA GCGTGGTAC CGTGGCGCTG	120
CGTGGGACCG CCAACCGCGGA TCCGGAGCCA GCGCCCGCGG TACCCACAAAC GCGCGCTCG	180
CGCGCGCTGA CGCGTGCAGC CGCACCGCGA CGGGCGACACG CTGGTGGCGCT CGCACCGCG	240